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/cgn2_6/ptodata/1/1na/6B_COMB.seq:US-09-107-847-1 + 31
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ysAspPheLeuLysAsnLeuProLysSerThrValAsnGlyValSerTrp
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; ORGANISM: Homo sapiens US-08-885-291-54
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; Sequence 54, Applicati
; Patent No. 6057125
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APPLICANT: Turek, Fred W.
APPLICANT: Pinto, Lawrence H.
TITLE OF INVENTION: CLOCK GENE AND GENE PRODUCT
FILE REFERENCE: 0290-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/08/885,291A CURRENT FILING DATE: 1997-06-30 EARLIER APPLICATION NUMBER: 08/816,693
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                                                                                                                                                                                                                                                    716 GAAACCTACA.....TTCCTTAGTAATGAAGAGTTTACACAATTAA
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                                                                                                                                                                                                                                                                                                                                                                                                                              uAspLeuValAsnThrSerValTyrAsnIleLeuHisGluGluAspArgL 167
                                                                                                      TGTTAGAGGCTCTTGATGGTTTTTTTTTAGCAATCATGACAGATGGAAGC
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                                                                                                                                                                                                                                                                                                                                             GAA....ATCACTGCACAGTCAGATGCTAGTGAAATTCGACAGGACTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAAAAGAAACGTAGAGATCAATTTAATGTTCTCATTAAAGAACTGGGATC
TGATCTTGTGGATCAAAGTATATTTAATTTTATCCCAGAAGGGGAACATT
                                                                                  ATAATATGTGTCTGAGAGTGTAACTTCATTACTTGAACATTTACCATC
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1520	IleArgProProMet	1507
ن	CATTATTATATCACTTACCAT	, ,
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236	ysPheAlaLeuSerGlnProArgAlaMetM	223
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223	MetArgGlnArgTyrGluTh	217
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216	IleLeuGluAspIleAsnAlaSerProGlu	207
1056	TAGACCCAAAGGAGCCATCTACCTATGAATATGTAA	1007
206	tLysThrProHisAsp	199
199	ThrasnGluProGlnArgGlnLysSerHisThrPheAsnCysArgMe:	184 957
956	CAGAGGTTTATAAAATACTCTCTACTCATCTGCTGGAAAGTGATTCATTA	907

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SerGlyValSerSerSerThrSerGlyGlyValSerSer 669	656 ro
CCCAGTCAGACACAGAGACACTCTTACAGCCC 2	60
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<pre>InLeuLeuThrCysSerSerAspAspArgGlyHisSerSerLeuThrAs 639</pre>	623 GlnL 2340
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622	606
<pre>rArgAspHisLeuSerAspLysGluSerLysGluSerSerValGluGlyA 606 : :: :: ::::::::::::::::::::::::::::</pre>	589 rArg ; 2270 AACT
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InProSerLysValSerAsnGlnAspSerLysSerProLeuGlyPheTyr 574 ::: ::::: :::	558 lnPr 2188 AACT
N) 17	38
GlyValGlyThrSerLeuLeuSerThrLeuSerSerProGly 545	532 2088 GTCC
TTCATCGGCAACAAGAAGAACTAAGAAAAATTCAAGAACAACTTCAGATG 2087	2038 TTCA
	531
nAlaIleSerGlu	527 nAla 1988 ACAT
HisserPheSerSerSerSerLeuSerAlaLeuGl :::: :::: ::: :TTTCAGTTTTCAGCTCAATTAGGAGCCATGCA	11 41
ACGAGCACTCCACCCAGGCAGCATTTACCAGCTCATGAGAAGATGGTGCA 1840	477 1791 ACGA
oGlyProGlyMetGlnSerProSerSerTyrGlnAsnAsnAsnTyrGlyL 461 ::: ::: :::::::::::::::::	444 oGly 1700 AACC
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PRIOR APPLICATION DATA: APPLICATION NUMBER: EP 97304996.8 PILING DATE: 08-UUI-1997 ATTORNEY_AGENT INFORMATION: NAME: Prestia, Paul F REGISTRATION NUMBER: 32,031 REFERENCE/DOCKET NUMBER: GH-30003 TELECOMMUNICATION INFORMATION: TELEPHONE: 610-407-0700 TELEFAX: 610-407-0701 TELEFAX: 610-407-0701 SEQUENCE CHARACTERISTICS: LENGTH: 5715 base pairs TYPE: nucleic acid	seq_documentation_block: Sequence 1, Application US/09107847 Patent No. 6100062 GENERAL INFORMATION: APPLICANT: DUCKWORTH, DAVID APPLICANT: MICHALOVICH, DAVID ITITLE OF INVENTION: NOVEL USE NUMBER OF SEQUENCES: 2 CORRESPONDENCE ADDRESS: ADDRESSEE: Ratner & Prestia STREET: P.O. Box 980 CITY: Valley Forge STATE: PA COUNTRY: USA ZIP: 19482 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/107,847 FILING DATE: 30-JUN-1998 CLASSIFICATION:			936 nSerMetGlyArgProGlyGlyAspTyrAsnThrSerLeuProArgProA 953 3013
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alignment_scores:
Quality: 313.00
Ratio: 0.607
Percent Similarity: 44.027
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                                                                                                                                                                                                                                                                           207 ......IleLeuGluAspIleAsnAlaSerProGlu 216
                                                                                                                                                                                                                                                                                                                                   842
                                                                                                                                                                                                                                                                                                                                                                     792 ACCCCAGAATATTTAAAATCAAAAAATCAGTTAGAATTCTGTTGTCACAT 841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            134 IleValPheValSerGluAsnValThrGlnTyrLeuGlnTyrLysGlnGl 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   592 TGTTAGAGGCTCTTGATGGTTTTTTTTTTAGCAATCATGACAGATGGAAGC 641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              117 euLeuGlnAlaLeuAspGlyPheLeuPheValValAsnArgGluAlaAsn 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100 lSerSerThrGlyGlnGlyValIleAspLysAspSerLeuGlyProLeuL 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              428 CATGCTTCCTGGTAATGCTAGA......AAGATGG
236 etGluGluGlyGluAspLeuGlnSerCysMetIleCysValAlaArgArg 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       184 ThrAsnGluProGlnArgGlnLysSerHis...ThrPheAsnCysArgMe 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       742 CAGAGGTTTATAAAATACTCTCTACTCATCTGCTGGAAAGTGATTCATTA 791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 167 ysAspPheLeuLysAsnLeuProLysSerThrValAsnGlyValSerTrp 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  551 GAAACCTACA.....TTCCTTAGTAATGAAGAGTTTACACAATTAA 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               507 GAA....ATCACTGCACAGTCAGATGCTAGTGAAATTCGACAGGACTG 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84 GluGlnGlyLysThrIleSerAsnAspAspAspValGlnLysAlaAspVa 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50 uLeuIleSerAlaAsnLeuSerAspIleAspAsnPheAsnValLysProA 67
                                                TAGAGTTTGTTTGTAGCTACTGTCAGGTTAGCTACACCTCAGTTCATCA 1041
                                                                                       rMetGlnCysPheAla.....LeuSerGlnProArgAlaMetM 236
                                                                                                                                                                                    .....MetArgGlnArgTyrGluTh 223
                                                                                                                                                                                                                                                                                                                                 GCTGCGAGGAACAATAGACCCAAAGGAGCCATCTACCTATGAATATGTAA 891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length: 1172
Gaps: 54
Percent Identity: 19.795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   456
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510	erHisGlnPheSerProValAlaGlyValHisSerProMetAlaSerSer	494
494 1725	nGlnAsnIleMetIleSerProArgAsnArgGlySerProLysIleAlas	477 1676
477 1675	ACGAGCACTCCACCCAGGCAGCATTTACCAGCTCATGAGAAGATGGTGCA	477 1626
476 1625	MețSerSerProProHisGlySerF ::::: TCAGACCCTTCCTCAACAC	461 1585
461 1584	OGlyProGlyMetGlnSerProSerSerTyrGlnAsnAsnAsnTyrGlyL 	444 1535
444 1534	AsnIleAlaSerLeuThrPr :: ATAAACACAGTCAGTCTCAAGGAAGCATTGGAAAGGTTTGATCACAGGCC	438 1485
437 1484	erThrThrGlyGlnMetSerGl :: :::::: AGACAGCTGCTGACAAAAGC	423 1441
423 1440	yLeuGlnMetProSerSerArgAlaTyrGlyLeuAlaAs ::::: AGTTAGGGCTGAAAGACGACGAGAACTTGGCATTGAAGA	408 1391
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375 1341	nAspArgHisGlyPheValSerThrHisPheLeuGl ::::::: 	358 1311
358 1310	IleValThrAlaGlnThrLysSerLysLeuPheArgAsnProValThrAs ::: TGGATTTGGCTTCAGACT	342 1293
341 1292	snGlyHisalaGluThrProValTyrArgPheSerLeuAlaAspGlyThr	325 1245
325 1244		308 1199
308 1198	GlyPheGluAspIleIleArgArgCysIleGlnArgPhePheSerLeuAs ::::: GGCTATGATTACTATCATGTGGA	292 1176
291 1175	LeuArgSerSerMetArgPro	285 1135
284 1134	rArgHisAspLeuSerGlyLysValValAsnIleAspThrAsnSer	269 1085
269 1084	IleThrThrGlyGluargThrPheProSerAsnProGluSerPheIleTh	253 1053
1052	AGGAA	1042

			2
	742	lnLeuSerProLysLysGluAsnAsnAlaLeuLeuArgTyrLeuLeu 	726
	2490	CAGGTGGTGACTGCATATCCTACTTTTGCTACACAACAGCAA	2441
	726	വ	719
	2440	GTGACTGCTCCTGTAGCTTGTGGGGCAGTCATGGTACCTAGTACTATGCT	2391
	718	rSerIleThr	710
	2390	AGGACAGGCAGATAAGATTTTCTCAAGGTCAACAACTTGTGACCAAATTA	2341
	709	·····AlaGlnAlaThrGlyLysAsp	703
	2340	TAGTATGCCACAAAACAGCACCCAGAGTGCTGCAGTAACTACATTCACTC	2291
	702	sLeuLeuGlnAsnGlyAsnSerProAlaGluValAlaLysIleTh	686
	2290		2268
	686	lySerLeuLeuGlnGluLysHisArg	670
	2267	CACTATGGTGATTTCTCAGCCTGCAG	230
	669	oSerGlyValSerSerShrSerGl	656
	2229	TCTACCCAGTCAGACACAGAGCACTCTTACAGCCC	195
	656	SerProLeuAspSerSerCysLysGluSerSerValSerValThrSe	639
	2194		175
	639	sSerSerLeuTh	623
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	2148	AACTCAGCACATGATACAACAACAGACTTTACAGAGTACATCAA	2105
	606	gAspHisLeuSerAspLysGluSerLysGluSerSerValGlu	589
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	589	roValGluSerSerMetCysGlnSerAsn	575
	2060	TTGCACCTATAAATATGCAAGGCCAAGTTGTT	2023
	574	GlnAsp	558
	2022	ΑŢ	1973
	558	ProLysLeuAspAsnSerProAsnMetAsnIleThrG	546
	1972	GTCCATGGTCAGGGGCTGCAGATGTTTTTGCAACAATCCAAATCCTGGGTT	1923
	545	alGlyThrSerLeuLeuSerThrLeuSerSerPro	532
	1922	AGAAAATTCAAGAACAACTT	1873
	531		531
	1872	ACATCTGAAAGACCAATTGGAACAACGGACACGCATGATAGAAGCAAATA	1823
	531	alle	527
		: :::::: :::::::::::::::::::::::::::::	1776
•	527	rAlaLeu	511
	1775	CATCATTAACACAGCCAGTGATGTCTCAAGCTACAAATTTACCAATTCCA	1726

3072	ASPOLYMELLEUSEIMEUSLUSLIIVALSEIHISGLYIIKGIIMSHAIGEF [GATGGAAAAAGAATATATTTGCCAAATA	3046
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997 2995	lyMetGlyAlaAsnP :::::: GGAGGTGATC	980 2964
980 2963	SerIleProGlyAlaArgProValLeuGlnGlnGlnGlnGlnGl	967 2914
966 2913	laLeuGlyGlySerIleProThrLeuProLeuArgSerAsn	953 2869
953 2868	nSerMetGlyArgProGlyGlyAspTyrAsnThrSerLeuProArgProA :::: ::: TaCTCAGATGACCTGAGGAAA	936 2848
936 2847	TrpGlyLeuProAsnSerLysalaGlyArgMetGluProMetAsnSerAs ::: :::	920 2812
2811	. '	2811
919	lyGlyProAsnArgAsnValThrValThrGlnThrProSerSerGlyAsp	903
903 2811	yGlyAsnProArgMetMetAspSerGlnGluAsnTyrGlySerSerMetG ::::::::::::::::::::::::::::::::::::	886 2779
886 2778	ValLysAsnIleSerAlaPheProMetLeuProLysGlnProMetLeuGl::::::::	870 2743
869 2742	euAspSerProValSerValGlySerSerProPro	858 2693
858 2692	SerGlnSerValGlnSerIleArgProPro.TyrAsnArgAlaValSerL::: :::	. 2643
841 2642	hrLysGlnGlnValPheGlnGlyThrAsnSerLeuGlyLeuLysSer 	826 . 2595
2594		2594
826	r Ser Asp Phe Tyr Asn Asn Ser I le Ser Ser Asn Gly Ser His Leu Gly Terminal Ser Asn Gly Ser Asn Gly Ser His Leu Gly Terminal Ser Asn Gly Ser Asn Gly Ser His Leu Gly Terminal Ser Asn Gly Se	809
2594		2594
809	${\tt GlySerGlyAspLeuAspAsnLeuAspAlaIleLeuGlyAspLeuThrSe}$	793
792 2594	erSerSarGlnGluLysAspProLysIleLysThrGluThrSerGluGlu : : : : : : : : :	776 2572
776 2571	IGluGlyValAspAsnLysMetSerGlnCysThrSerSerThrIlePros ::: ::::::::: :::	759 2528
759 2527	AspArgAspAspProSerAspAlaLeuSerLysGluLeuGlnProGlnVa	. 743 2493

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US-09-041-994-2 x US-08-816-693A-1
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Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                  ; NAME/KEY:
; LOCATION:
US-08-816-693A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_documentation_block:
; Sequence 1, Applicatio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: /cgn2_6/ptodata/1/ina/5B_COMB.seq:US-08-816-693A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5874241 http:// Thomas E
REGISTRATION NUMBER: 33,268
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 7498 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: 11near
                                                                                                                                                                                                        Align seg 1/1 to: US-08-816-693A-1
                                                                                                                                                                                                                                                                                                         Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          equence 1, Application US/08816693A
tent No. 5874241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3113 AAGGCACTAATGAT 3126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1045 luGlyGlnSerAsp 1049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/816,693A
FILING DATE:
FILING DATE:
                                                                                                                    APPLICANT: Takahashi, Joseph S
APPLICANT: Turek, Fred W
APPLICANT: Turek, Fred W
APPLICANT: Pinto, Lawrence H
TITLE OF INVENTION: Clock Gene and Gene Product
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Rockey, Milnamow & Katz
STREET: Two Prudential Plaza, Suite 4700
                                      565 TATGCTTCCTGGTAACGCGAGA.....AAGATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA (genomic) FEATURE:
67 spLysCysAlaIleLeuLysGluThrValArgGlnIleArgGlnIleLys 83
                                                                              50 uLeuIleSerAlaAsnLeuSerAspIleAspAsnPheAsnValLysProA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: Two Prud
CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 60601
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDS
389..2954
                                                                                                                                                                                                                                                                                                         309.50
0.614
44:288
                                                                                                                                                                                                                                                                                                         Percent Identity: 19.947
                                                                                                                                                                                                        from: 1 to: 7498
                                          593
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325 138 341	pSerGlnLys ::::: GGCAAAATGT hrProValTy ::
\vdash ω	292 GlyPheGluAspIleIleArgArgCysIleGlnArgPhePheSerLeuAs :::: 1313 GGCTATGATTACTATCATGTGGA
1 2	285LeuArgSerSerMetArgPro
μ N	269 rArgHisAspLeuSerGlyLysValValAsnIleAspThrAsnSer : :::
H 2	GlyGluArgThrPhe
252 118	236 etGluGluGlyGluAspLeuGlnSerCysMetIleCysValAlaArgArg
23 11	LeuSerGlnProAr ::: :: NGATTAGCTACACCTCA
22 11	MetargGlnargTyr
21 10	TTTTAA
20 10	ProHisAsp
19 97	. Thr I
18 92	167 ysaspPheLeuLysasnLeuProLysSerThrValasnGlyValSerTrp
16 87	150 uAspLeuValAsnThrSerValTyrAsnIleLeuHisGluGluAspArgL
15 82	134 IleValPheValSerGluAsnValThrGlnTyrLeuGlnTyrLysGlnGl :::::: ::: :::
13 77	117 euLeuGlnAlaLeuAspGlyPheLeuPheValValAsnArgGluAlaAsn :: ::: :::::::::::::
11 72	100 lSerSerThrGlyGlnGlyValIleAspLySAspSerLeuGlyProLeuL ::: :::::::::::::::::::::::::::
100	lyLysThrIleSerAsnAspAspAspV:
a	

ō		2019
627	rLysGlyHisLysLysLeuLeuGlnLeuLeuThrCys	611
611 2018	raspLysGluSerLysGluSerSerValGluGlyAlaGluAsnGlnArgG : ::: :::::::::: ::: ::: AGACCAGCTAGAGCAGCGGACACGGATGATAGAGGCAAATATTCATCGGC	594 1969
1968	GCCATGCAGCATCTAAA	
594	rArgAspHisLeuSe	578
1951	::: ::: CATGTCACAGTTTCAGTTTTCAGCTCAGTTAGGA	1917
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1916	AGCGATGTCTCAAGCTGCAAATTTACCAATTCCACAAG	1877
561	lyProLysLeuAspAsnSerProAsnMetAsnIleThrGlnProSerL	544
1876		1847
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7		1722
477	AsnMetSerSerProProHisGlySerProGlyLeuAlaProAsnGln	461
1721	IOSELSELLYIGIUASUASUASUIYIGIYL	
101	Drock what Claser Drocerser Turck a sententury of ut	444
444 1671	AsnIleAlaSerLeuThrPr ::: ::: ATCAACACAGTGAGTCTCAAGGAAGCACTGGAAAGGTTTGATCACAGCCC	438 1622
1621	acagctgctgacaaaagccaagattctgggtctgacaatcgt	7
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408	CysAsnSerSerValGlyGlyMetSerMetSerProAsnGlnGl	392
1492		7
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375 1478	naspargHisGlyPheValSerThrHisPheLeuGinargGligGlnAsnG	358 1448
4	GUATATIGGCTTCAGACT	۱ (
358	leValThrAlaGlnThrLysSerLysLeuPheArgAsnProValThrAs	342
1429	GGAAAAGGCAAATCGTGTTACTATAGATTCCTGACCAAAGGCCAGGCAG	1382

926 2491	hrValThrGlnThrProSerSerGlyAspTrpGlyLeuProAsnSerLys :::::	910 2442
910 · 2441	PSerGlnGluAsnTyrGlySerSerMetGlyGlyProAsnArgAsnValTIII::::::::::::::::::::::::::::::::::	893 2396
893 2395	PrometLeuProLysGlnPrometLeuGlyGlyAsnProArgmetMetAs ::: :: ACGATGGTGATTTCCCAGCCTGCAGCTGGG	. 877 2366
876 2365	erProValSerValGlySerSerProProValLysAsnIleSerAlaPhe	860 2328
860 2327	nSerValGlnSerIleArgProProTyrAsnArgAlaValSerLeuAspS ::: ::::::::::::: 	843 2278
843 2277	LysGlnGlnValPheGlnGlyThrAsnSerLeuGlyLeuLysSerSerGl::: ::: ::: ::: ::: ::::: ::: CAGCAACAGACTTTACAAAGTACATCA	827 2243
826 2242	erAspPheTyrAsnAsnSerIleSerSerAsnGlySerHisLeuGlyThr :: ::	810 2222
810 2221	ySerGlyAspLeuAspAsnLeuAspAlaIleLeuGlyAspLeuThrSerS 	793 2210
793 2209	SerSerGlnGluLysAspProLysIleLysThrGluThrSerGluGluGl :::::: AACCAGGTTCAG	777 2198
2197	::: ::: GTCCCTGCT	2189
2188 776	luGlvValAspAspLvsMetSerGlnCvsThrSerSerThrIleProSer	2168 760
760	pArgAspAspProSerAspAlaLeuSerLysGluLeuGlnProGlnValG	743
743 2167	LeuSerProLysLysCluAsnAsnAlaLeuLeuArgTyrLeuLeuAs	727 2159
726 2158	erSerIleThrSerCysGlyAspGlyAsnValValLysGlnGluGln :: ::: :::: ::: grectgrecactttcctctggaaattctaatatccagcag	711 2118
711 2117	rProAlaGluValAlaLysIleThrAlaGlnAlaThrGlyLysAspThrS :::	694 2102
694 2101	LeuGlnGluLysHisArgIleLeuHisLysLeuLeuGlnAsnGlyAsnSe	678 2075
677 2074	erSerThrSerGlyGlyValSerSerThrSerAsnMetHisGlySerLeu ::: :: GTCCATGGTCAAGGG	661 2060
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661	${\tt rSerCysLysGluSerSerValSerValThrSerProSerGlyValSerS}$	644
2059		2059
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; ORGANISM: Mus musculus US-08-885-291-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: /cgn2_6/ptodata/1/ina/6A_COMB.seq:US-08-885-291-1
                                           SOFTWARE: Patentin Ver.
SEQ ID NO 1
LENGTH: 7498
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/08885291A Patent No. 6057125 GENERAL INFORMATION:
                                                                                                                                            CURRENT APPLICATION NUMBER: US/08/885,291A CURRENT FILING DATE: 1997-06-30 EARLIER APPLICATION NUMBER: 08/816,693 EARLIER FILING DATE: 1997-03-13 NUMBER OF SEQ ID NOS: 55
                                                                                                                                                                                                                                                                 APPLICANT: Takahashi, Joseph S.
APPLICANT: Turek, Fred W.
APPLICANT: Pinto, Lawrence H.
TITLE OF INVENTION: CLOCK GENE AND GENE PRODUCT
FILE REFERENCE: 0290-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2980
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3030 GAAGTTGAACAG 3041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1044
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2583 CTGCCTATCCTACCTTCGCCACACACAGCAGCAGGCACAG...ACATTA 2629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 973 ProValLeuGlnGlnGlnGlnGlnMetLeuGlnMetArgProGlyGluI1 989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        927
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCGAGAGGAAGGAATGGCCAGAAAGAATCGCTCAGTTGGCATGCGGTCA 3029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hrAspAlaThrGlyLeuGluGluIleAspArgAlaLeuGlyIleProGlu 1080
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LeuValAsnGln 1084
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alignment_scores

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alignment_block:
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                                                                                                                                                                                                                                                                                                                               1079 AATGGTTTTGAAGGAACTATACAACGCACACATAGGCCTTCTTATGAAGA 1128
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                                                                                                                                                              236 etGluGluGlyGluAspLeuGlnSerCysMetIleCysValAlaArgArg 252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      565 TATGCTTCCTGGTAACGCGAGA.....AAGATGG
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                                              IleThrThrGlyGluArgThrPheProSerAsnProGluSerPheIleTh 269
                                                                                                                                                                                                                                                                        rMetGlnCysPheAla.....LeuSerGlnProArgAlaMetM 236
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Percent Identity: 19.947
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544 187	AlaIleSerGluGlyValGlyThrSerLeuLeuSerThrLeuSerSerPr !	528 1847
527 1846	erSerSerSerLeuSerAlaLeuGln ::: ::::: GCAGTCAGTCCATAAAC	511 1806
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494 1783	ysIleAlaSe	478 1763
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461 172:	<pre>yrGlnAsnAsnTyrGlyL ::::::::::::::::::::::::::::::::::::</pre>	444 1672
444 167:	AsnIleAlaSerLeu	438 1622
437 162)	.laArgTyrGlyGlySerSer ::: .:: ::: CAAGATTCTGGGTCTGACAATCGT	423 1578
423 1577	yLeuGlnMetProSerSerArgAlaTyrGlyLeuAlaAspProS.;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;	408 1528
408 152	nGlnGl	392 1493
391 1497	rArgProAsnProAsnProValGlyGlnGlyIleArgProProMet ::: AGGCCAGAGTTC	375 1479
375 147	euGlnArgGluGlnAsnG : CAGTGGAATT	358 1448
358 1447	IleValThrAlaGlnThrLysSerLysLeuPheArgAsnProValThrAs ::: TGGATATGGCTTCAGACT	342 1430
341 1429	Thr	325 1382
325 1381	ArgHisTyrGlnGluAlaTyrLeuA ::::::: CACGAGCACTTAATGCAATAT	308 1336
308 1335	GlyPheGluAspIleIleArgArgCysIleGlnArgPhePheSerLeuAs :::::	292 1313
291 1312	CAATAATAGGCTATTTGCCATTTGAAGTCTTGGGAACATCA	285 1272
284 1271	rArgHisAspLeuSerGlyLysValValAsnIleAspThrAsnSer : ::: ::: TAGACACAGTTTAGAATGGAAGTTTCTATTTTTAGATCACAGGGCACCAC	269 1222

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843	827 2243	810 2222	793 2210	777 2198	760 2189	743 2168	727 2159	711 2118	694 2102	678 2075	661 2060	2059	644	2059	628	611 2019	594 1969	578 1952	561 1917	1877
nSerValGlnSerIleArgProProTyrAsnArgAlaValSerLeuAspS 	LysGlnGlnValPheGlnGlyThrAsnSerLeuGlyLeuLysSerSerGl:::: :::: :::: ::::: CAGCAACAGACTTTACAAAGTACATCAACTCAGCA	erAspPheTyrAsnAsnSerIleSerSerAsnGlySerHisLeuGlyThr ::: ::: AGCACAGGCCAGCACATGATA	ySerGlyAspLeuAspAsnLeuAspAlaIleLeuGlyAspLeuThrSerS 	SerSerGlnGluLysAspProLysIleLysThrGluThrSerGluGluGl:::: AACCAGGTTCAG	luGlyValAspAsnLysMetSerGlnCysThrSerSerThrIleProSer ::: ::: GTCCCTGCT	pArgAspAspProSerAspAlaLeuSerLysGluLeuGlnProGlnValG 	LeuSerProLysLysCluAsnAsnAlaLeuLeuArgTyrLeuLeuAs	erSerIleThrSerCysGlyAspGlyAspNalValLysGlnGluGln :: :::	rProAlaGluValAlaLysIleThrAlaGlnAlaThrGlyLysAspThrS	LeuGlnGluLysHisArgIleLeuHisLysLeuLeuGlnAsnGlyAsnSe 	erSerThrSerGlyGlyValSerSerThrSerAsnMetHisGlySerLeu ::: ::: GTCCATGGTCAAGGG		rSerCysLysGluSerSerValSerValThrSerProSerGlyValSerS		SerSerAspAspArgGlyHisSerSerLeuThrAsnSerProLeuAspSe	lyProLeuGluSerLysGlyHisLysLysLeuLeuGlnLeuLeuThrCys :::: ::: ::: :::	rAspLysGluSerLysGluSerSerValGluGlyAlaGluAsnGlnArgG :::	AsnProValGluSerSerMetCysGlnSerAsnSerArgAspHisLeuSe	ysValSerAsnGlnAspSerLysSerProLeuGlyPheTyrCysAspGln 	
860	843 2277	826 2242	810 2221	793 2209	776 2197	760 2188	743 2167	726 2158	711 2117	694 2101	677 2074	2059	661	2059	644	627 2059	611 2018	594 1968	577 1951	1916

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seq_documentation_block:
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                Sequence 1, Application US/08227536 Patent No. 5658784 GENERAL INFORMATION:
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APPLICANT:
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Eckner, Richard
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; NAME/KEY:
; LOCATION:
US-08-227-536-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: US-08-227-536-1 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-041-994-2 x US-08-227-536-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMUNICATION INFORMATION:
TELEPHONE: (617) 542-2290
TELEFAX: (617) 451-0313
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 9046 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HYPOTHETICAL: I
ANTI-SENSE: NO
FRAGMENT TYPE:
FEATURE:
                                                                                                                                                                                                                              6562 TCTGCTGCTACCATGCCAAGCACTGCCAGGAGAACAAATGCCCGGTGCCG 6611
                                                                                                                                                                                     802 laIleLeuGlyAspLeuThrSerSerAspPheTyrAsnAsnSerIleSer 818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/227,536
FILING DATE: 14 APPR 1994
CLASSIFICATION: 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Ewen, Mark
APPLICANT: Livingston, David
TITLE OF INVENTION: NUCLEIC ACID, ENCODING TRANSCRIPTION
TITLE OF INVENTION: FACTOR P300 AND USES OF P300
                                                                                                                                                                                                                                                                       786 sThrGlu...ThrSerGluGluGlySerGlyAspLeuAspAsnLeuAspA 802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Williams Ph.D., Kathli
REGISTRATION NUMBER: 34,380
REFERENCE/DOCKET NUMBER: DEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                   770 ThrSerSerThrIleProSerSerSerGlnGluLysAspProLysIleLy 786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                 SerAsnGlySerHisLeuGlyThrLysGlnGlnValPheGlnGlyThrAs 835
CAGGGCCTCCCTTCCCCCACTCCTGCCACTCCAACGACACCAACTGGCCA
                                nSerLeuGlyLeuLysSerSerGlnSerValGln.....S
                                                                            TTCGCAGGAGGATGGCCAGCATGCAGCGGACTGGTGTGGTTGGGCAGCAA 673:
                                                                                                                                                        .....AGCAACAGCTGCAGCACCGAC...TACAGCAGGCCCAAATGC 668:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality:
Ratio:
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1200..8441
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           274.00
0.828
47.353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length: 699
Gaps: 29
Percent Identity: 23.176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DFCI-308XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Version #1
                                                                                                                                                                                                                                                                                                                                                                                             ţo:
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                                     847
  6781
                                                                                                                                                                                                                                    6642
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861 ProvalservalclySerSerPropro.ValLysAsnileSerAlaPhep 87 1	847 6782	8 :	360 5831
	ωδ	roValSerValGlySerSerProPro.ValLysAsnIleSerAlaPheP :::	377
882 ÓCTGTGTCCÓA. 884 SerGlnGluAsnTyrGlySerSerMetGlyGlyProAsnArgAsnValTh 893	77	ıProLysGlnProMetLeuGlyGlyAsnProArgMetMetAsp :	œ
894 SergingluasnTyrglySerSerMetGlyGlyProAssnAryAsnValTh 893	882	3CCA	89
910 rValThrGinThProSerSerGlyAspTrpGlyLeuProAsnSerLysA 9 910 rValThrGinThProSerSerGlyAspTrpGlyLeuProAsnSerLysA 9 923	89	erGlnGluAsnTyrGlySerSerMetGlyGlyProAsnArgAsnValTh	10
910 FVAITHTGINTPPOSETSETGLYASPTFPGLYLEUPPOARSETLYSA 922	o ā	VI I II LO I II	2 2
927 laGlyArgMetGluProMetAsnSerMetGlyArgProGlyGly 996 CCCCCACCTACAGCAGTGGAAATTGCAATTGCAATTCAGAGAGAG	923	rvalThrGinThrProSerSerGlyAspTrpGlyLeuProAsnSerLysA :::	27 95
960 CCCCCACCTACAGCAGTGGAATGGCAATGCAGATTCAGAGAGCAGCGGA 944 ASPTYRASNThrSerLeuProArgProAlaLeuGlyGlySerIleProTh 941	92	aGlyArgMetGluProMetAsnSerAsnSerMetGlyArgProGlyGly	43
944 ASPTYRASNThrSerLeuProArgProAlaLeuGlyGlySerIleProTh	96	CCCCACCTACAGCAGTGGAAATGGCAATGCAGATTCAGAGAGCAGCGGA	0
960 rLeuProLeuArgSerAsnSerIleProGlyAlaArgProValL	944 7010	PTyrAsnThrSerLeuProArgProAlaLeuGlyGlySerIleProTh	05
975 euGlnGlnGlnGlnGlnMetLeu.GlnMetArgProGlyGluIleProMe ::::: :::::::::	ש פ	LeuProLeuArgSerAsnSerIleProGlyAlaArgProValL :::: ::::	75
110 CCCATGACCACAGGTCCCAGTTGGGCATTTGGAGCCAGGGATGGGATCGGACCGAC 991 tGlyMetGlyAlaAsnProTyrGlyGlnAlaAlaAlaAserAsnGlnLeuG 1	7	lnGlnGlnGlnMetLeu.GlnMetArgProGlyGluIleProMe	9
991 tGlyMetGlyAlaAsnProTyrGlyGlnAlaAlaAlaSerAsnGlnLeuG	7110	CATGACCAGAGGTCCCAGTGGGCATTTGGAGCCAGGGATGGGACCGAC	15
008 lySerTrpProAspGlyMetLeuSerMetGluGlnValSerHisGlyThr 1	991 7160	lyMetGlyAlaAsnProTyrGlyGlnAlaAlaAlaSerAsnGlnLeuG GGATGCAGCAACAGCCA	178
179CCCTGGAGCCAAGGATTGCCTCAGCCCAGCAACTACAGTCTGGG 179CCCTGGAGCCAAGGAGGATTGCCTCAGCCCAGCAACTACAGTCTGGG 1025 GlnAsnArgProLeuLeuArgAsnSerLeuAspAspLeuValGlyProPr 1	8001	SerTrpProAspGlyMetLeuSerMetGluGlnValSerHisGlyThr	0
### ### ### ### ### ### ### ### ### ##	N ~	CCTUGAGCAAGGAGGATTGCCTCAGCCCCAGCAACTACAGTCTGGG AsnArgProLeuLeuArgAsnSerLeuAspAspLeuValGlyProPr	1226
041 oSerAsnLeu	N	CCAAGGCCAGCCATGATGTCAGTGGCCCAGCATGGTCAACC	27
271 TTTGAACATGGCTCCACAACCAGGATTGGGCCAGGTATCAGCCCAC 73 045GluGlyGlnSerAspGluArgAlaLeuLeuAspGlnLeuHisThr 10 141	حة ا	AsnLeu	0
045GluGlyGlnSerAspGluArgAlaLeuLeuAspGlnLeuHisThr 10	7271	AACATGGCTCCACAACCAGGATTGGGCCAGGTAGGTATCAGCCCAC	7320
060 LeuLeuSerAsnThrAspAlaThrGlyLeuGluGluIleAspArgAlaLe 10	3 0	GluGlyGlnSerAspGluArgAlaLeuLeuAspGlnLeuHisThr 	1370
371 CTCAGGTCTCCCAGCTCTCCCCTGCAGCAGCAGCAGCAGGTGCTTAGTATCCT 74 076 uGlyIleProGluLeuValAsnGlnGlyGlnAlaLeuGluProLysG 10	06	LeuSerAsnThrAspAlaThrGlyLeuGluGluIleAspArgAlaLe	07
076 uGlylleProGluLeuValAsnGlnGlyGlnAlaLeuGluProLysG 10	37	AGGTCTCCCAGCTCTCCCCTGCAGCAGCAACAGGTGCTTAGTATCCT	7420
092 lnAspAlaPheGlnGlyGlnGluAlaAlaValMetMetAspGlnLysAla 11 443	07	GlyIleProGluLeuValAsnGlnGlyGlnAlaLeuGluProLysG ::: ::: ::: CACGCCAACCCCCAGCTGTTG	L092 7442
443	1092	AspAlaPheGlnGlyGlnGluAlaAlaValMetMetAspGlnLysAla	_
109 GlyLeuTyrGlyGlnThrTyrProAlaGlnGlyPro	7443		46
*O/ GCCOOLINGC	6 0	LaGlnGlyPro	12

1376 8332	AsnLeuAlaArgAsnSerSerPheSerGlnGlnGlnPheAlaHisGlnGl::::::::::::::::::::::::::::::::::	1360 8295
1359 8294	GlnSerSerGluMetLysGlyTrpProSerGly :::: :::: ::::	1349 8245
1348 8244	yProSerGlnAsnProMetMetGlnHisProGlnAlaAlaSerIleTyr. :::::	1332 8195
1332 8194	PheGlyArgValSerSerProProAsnAlametMetSerSerArgMetGl	1316 8145
1315 8144	heProTyrGlnProAsnTyrGlyMetGlyGlnGlnProAspProAla :: ::	1300 8095
1300 8094	tAspGlyLeuLeuAlaGlyProThrMetProGlnAlaProProGlnGlnP:::	1283 8081
1283 8080	PheSerProProProAsnValThrAlaSerProSerMe ::: ::: ATGAGCCCCCAGCAGCATATGCTCCCAAATCAGGCCCAGTCCCCACACCT	1271 8031
1270 8030	InGinGinGinGinGinGinGinGinGinGinGinThrGinAla	125 4 7981
1254 7980	nGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnG	1247 7931
1247 7930	SerHisHisPheArgGlnGlnArgValAlaMetMetMetGlnGlnGlnGl::: ::::	1231 7881
1230 7880	InGlyPheLeuAsnAlaGlnMetValAlaGlnArgSerArgGluLeuLeu	1214 7843
121 4 7842	nProThrAlaGlyGlyAlaAlaValMetArgProMetMetGlnProGlnG:	1197 7793
1197 7792	: 12	1181 7755
1180 7754	snThrProLysGlnLeuArgMetGlnLeuGlnGlnArgLeuGlnGly	1165 7717
1165 7716	eProLeuGlnGlyMetHisProArgĀlaAsnIleMetArgProArgThrA ::: ::: ::: ::: ACCCATGGGAGGGATGAGCCCCCAGGCTCAGCAGATGAACATGAACCACA	1148 7667
1148 7666		1139 7617
1138 7616	lyPheHisLeuGlnGlyGlnSerProSerPheAsnSerMet	1125 7567
1125 7566	GCCCCAGGGGCAGCCAGGGCTACAGCCATGCCATGCCAGGTCAGCAGG	1121 7517

1376 yAsnProAlaValTyrSerMetValHisMetAsnGlySerSer 1390

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alignment_block:
US-09-041-994-2 x PCT-US95-04682-1
                                                                                                                                                                                                                                                                                                         alignment_scores:
Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_documentation_block:
; Sequence 1, Application PC/TUS9504682
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:PCT-US95-04682-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: DFCI-308Xq999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-2290
TELEPAX: (617) 451-0313
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 9046 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                   Align seg 1/1 to: PCT-US95-04682-1 from: 1
                                                                                                                                                                                                                                                                         Ratio:
Percent Similarity:
                                                                                                          MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE. ...
                                                          786 sThrGlu...ThrSerGluGluGlySerGlyAspLeuAspAsnLeuAspA 802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Weingarten, Schurgin, Gagnebin & Hayes
STREET: Ten Post Office Square
802 laIleLeuGlyAspLeuThrSerSerAspPheTyrAsnAsnSerIleSer 818
                                                                                                                                                                                                                                                                                                                                                                                                                                          ANTI-SENSE:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Holliday C. Heine, Ph.D.
REGISTRATION NUMBER: 34,346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,536
FILING DATE: 14-April-1994
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: Ten P
CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: PCT/US95/04682 FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . אא
US
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1200..8441
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0.828
47.353
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                                                                                                                                                                                                                                                                     Length: 699
Gaps: 29
Percent Identity: 23.176
                                                                                                                                                                                   to: 9046
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1076 uGlyIleProGluLeuValAsnGlnGlyGlnAlaLeuGluProLysG 1092
1060 LeuLeuSerAsnThrAspAlaThrGlyLeuGluGluIleAspArgAlaLe 1076
1045GluGlyGlnSerAspGluArgAlaLeuLeuAspGlnLeuHisThr 1059
1041 oSerAsnLeu
snArgProLeuLeuArgAsnSerLeuAspAspLe
1008 lySerTrpProAspGlyMetLeuSerMetGluGlnValSerHisGlyThr 1024 :: :: :: 7179CCCTGGAGCCAAGGAGTGCCTCAGCCCCAGCAACTACAGTCTGGG 7226
GlyAlaAsnProTyrGlyGlnAl ::: CAGCAACAGCCA
975 euGlnGlnGlnGlnMetLeu.GlnMetArgProGlyGluIleProMe 991
960 rLeuProLeuArgSerAsnSerIleProGlyAlaArgProValL 975
944 AspTyrAsnThrSerLeuProArgProAlaLeuGlyGlySerIleProTh 960
927 laGlyArgMetGluProMetAsnSerAsnSerMetGlyArgProGlyGly 943
910 rValThrGlnThrProSerSerGlyAspTrpGlyLeuProAsnSerLysa 927 :::
894 SerGlnGluAsnTyrGlySerSerMetGlyGlyProAsnArgAsnValTh 910 :::
877 roMetLeuProLysGlnProMetLeuGlyGlyAsnProArgMetMetAsp 893 ::: 6882 CCTGTGTCCCA
861 ProValSerValGlySerSerProPro.ValLysAsnIleSerAlaPhep 877
847 erIleArgProProTyrAsnArgAlaValSerLeuAspSer 860 :: ::: ::: ::: :::
835 nSerLeuGlyLeuLysSerSerGlnSerValGln
819 SerAsnGlySerHisLeuGlyThrLysGlnGlnValPheGlnGlyThrAs 835
6643AGCAACAGCTGCAGCACCGACTACAGCAGGCCCAAATGC 6681

1247

7881

1214

7567

50 uLeuIleSerAlaAsnLeuSerAspIleAspAsnPheAsnValLysProA 67 :::::: :::
34 GluLysargargargaluGlnGluSerLysTyrIleGluGluLeuAlaGl 50
Align seg 1/1 to: US-08-785-310A-4 from: 1 to: 4184
alignment_block: US-09-041-994-2 x US-08-785-310A-4
alignment_scores: Quality: 264.00 Length: 1017 Quality: 0.532 Gaps: 53 Percent Similarity: 48.771 Percent Identity: 21.141
: TYPE: DUCLELC ACID ; STRANDEDNESS: double ; TOPOLOGY: linear ; MOLECULE TYPE: CDNA US-08-785-310A-4
H: CE C
; TELECOMMUNICATION INFORMATION: : TELEPHONE: (415) 343-4341 ; TELEFAX: (415) 343-4342
REGISTRATION NUM REFERENCE/DOCKET
536 FORMATION
CURKENT APPLICATION DATA: APPLICATION NUMBER: US/08/785,310A FILING DATE: 21-JAN-1997
TER: IBM PC composition SYSTEM: PC-I
)4 ADABLE FORM: PE: Floppy disk
CITY: SAN FRANCISCO STATE: CALIFORNIA COUNTRY: USA
; ADDRESSE: SCIENCE & TECHNOLOGY LAW GROUP ; ADDRESSE: SCIENCE & TECHNOLOGY LAW GROUP ; STREET: 268 BUSH STREET, SUITE 3200
GENERAL INFORMATION: APPLICANT: McKnight, Stev
seq_documentation_block: ; Sequence 4, Application US/08785310A
seq_name: /cgn2_6/ptodata/1/ina/5B_COMB.seq:US-08-785-310A-4
1376 yAsnProAlaValTyrSerMetValHisMetAsnGlySerSer 1390
1360 AsnLeuAlaArgAsnSerSerPheSerGlnGlnGlnPheAlaHisGlnGl 1376 ::: ::: ::: 8295 AGCCCGGACCAGAATTCAATGCTTTCTCAGCTT
1349GlnSerSerGluMetLysGlyTrpProSerGly 1359

67 703	sAlaIleLeuLysGluThrValArgGlnIleArgGlnIleLys ::::::: :::::::::::::::::::::::::::	83 752
84 753	.nGlyLysThrIleSerAsnAspAspAspValGlnLysAlaAspVa ::: ::: :::::: ::: ::: GTCTCAGCACAAACAGAAATCTGTGACAT	100 784
100 785	hrGlyGlnGlyValIleAspLysAspSerLeuGlyProL 	116
116 835	aLeuAspGlyPheLeuPheValValAsnArgGluAla ATTAGATGGCTTCGTCATCGTCGTGACAACAGACGGC	132 884
133 885	lnTyrLeuGlnTyrLysGl CTCTCCTTGGACATTTACC	149 934
149 935	SerValTyrAsnIleLeuHisGluGluAspA ::::: ::: ::::: AACTTGTTAAATTTCCTTCCAGAGCAAGAAC	166 984
166 985	heLeuLysAsnLeuProLysSerThrValAsnGlyValSer	182 1028
183 1029	yGlnLysSerH1sThrPheAs 	196 1078
196 1079	COH1SASPIleLeuGluASPIleASNA:::: AGCT	213 1101
213 1102	ArgTyrGluThrmetGlnCysPhe 	227 1151
227		227
1152	TTCGCTCTTACAACAATGTGCCTAGCCCCTCCTGTAATGGCTTTGACAA	1201
0		N .
244 1245	SMETILECYSVALALAARGARGILEThrThrGlyGlu ::: ::::::::: 	257 1292
258 1293	gThrPheProSerAsnProGluSerPheIleThrArgHisAspLe GTGTGTAGCTGACGAACCTTTAGAGGAATTCACTTCGAGGCATAGCTT	273 1342
273 1343	lyLysValValAsnIleAspThrAsnSer	284 1392
285 1393	LeuArgSerSerMetArgProGlyPheGlu	294 1433
295 1434	AspileileargargCysileGlnargPhePh :::::::	305 1483
305 L484	eSerLeuAsnAspGlyGlnSer	312 1533

616	luSerSerValGluGlvAlaGluAsnGlnArgGlvProLeuGluSerLvs	600
2154	GATCCTGCAGGCCAACATTCGGTGGCAGC	2126
600	tCysGlnSerAsnSerArgAspHisLeuSerAspLysGluSerLysG	583
2125		2103
583		. 567
2102	TTTCAGCACAATTCAGCATGTTCCAGACCATTAAA	2068
566	_	550
550 2067	lGlyThrSerLeuLeuSerThrLeuSerSerProGlyProLysLeuAspA ::: ::: ACCGGCTTGCAGAGTCCACCTGCTCCAGTGACACAGT	533 2031
533 2030	SerSerSerLeuSerAlaLeuGlnAlaIleSerGluGlyVa :: ::	520 1986
519 1985		503 1942
503 1941	nArgGlySerProLysTleAlaSerHisGlnPheSerProValAlaGlyV	486 1907
486 1906	SerProGlyLeuAlaProAsnGlnGlnAsnIleMetIleSerProArgAs ::: ::::::: ACTCCAACCAAGCTGATGGCTGAGAACAGCACACGCTTTGCCAAGACC	470 1857
469 1856	erTyrGlnAsnAsnAsnTyrGlyLeuAsnMetSerSerProProHisGly	453 1816
453 1815		436 1769
1768	HIAMSPETOSETTHTTHTGLYGIMECSETSLYMIAKTGTYFGLYGLYSE	1764
1763		1740
419	roSerSerArgAlaTyrGlyLeu	403
403 1739	yIleArgProProMetAlaGlyCysAsnSerSerValGlyGlyMetSerM :::::: CCTAGAGCCTCCA	386 1727
386 1726	GlnAsnGlyTyrArgProAsnProAsnProValGlyGlnGl	373 1698
1697		1681
370		1 A C
356 1680	YThrIleValThrAlaGlnThrLysSerLysLeuPheArgAsnProV ::: :::::: CGCAGATGTTTGGAGAGAGAGAGAGAGAGCTTGGGAGAGAGA	340 1631
340 1630	LeuAsnGlyHisAlaGluThrProValTyrArgPheSerLeuAlaAspGl :::	324 1581
323 1580	TrpSerGlnLysArgHisTyrGlnGluAlaTyr	313 1534

05	<pre>89 roArgMetMetAspSerGlnGluAsnTyrGlySerSerMetGlyGlyPro 9</pre>	
936	72 nIleSerAlaPheProMetLeuProLysGlnProMetLeuGlyGlyAsnP 8 :: :: :: 12 TCTCTCCACCTTCTCCCAGCAGCCG	87 291
72 911	57 SerLeuAspSerProValSerValGlySerSerProProValLysAs 8 :::: ::: ::: :: :	85 286
56 86,4	40 ysSerSerGlnSerValGlnSerIleArgProProTyrAsnArgAlaVal 8 :: :: ::: :::	84 283
40 829	27 SGlnGlnValPheGlnGlyThrAsnSerLeuGlyLeuL 8	82 278
780	11 AspPheTyrAsnAsnSerIleSerSerAsnGlySerHisLeuGlyThrLy 8	81 273
10 735	94 erGlyAspLeuAspAsnLeuAspAlaIleLeuGlyAspLeuThrSerSer 8 ::: ::::::::::::::::::::::::::::::::	79 268
94	77 rSerGlnGluLysAspProLysIleLysThrGluThrSerGluGluGlyS 7 :::::: ::: ::: :::	
777 2644	65 LysMetSerGlnCysThrSerSerThrIleProSerSe ::: ::: :5 CAGCTCAGGCTGTTGCTGAGCCAGCCCATCCAGCCTATGATGCCTGGGTC	76 259
764 2594	49 spAlaLeuSerLysGluLeuGlnProGlnValGluGlyValAspAsn	74 255
49	32 sGluAsnAsnAlaLeuLeuArgTyrLeuLeuAspArgAspAspProSerA 7 :	73 250
32 500	16 CysGlyAspGlyAsnValValLysGlnGluGlnLeuSerProLysLysLy 7	71 248
15	99 laLysIleThrAlaGlnAlaThrGlyLysAspThrSerSerIleThrSer 7 :::::::	69 243
699 2433	82 sArgileLeuHisLysLeuLeuGlnAsnGlyAsnSerProAlaGluValA : ::: ::: ::: 96 TGTGATATCCGCCCAGGGTCCAAAGCCAATGAGAAGTT	
82 395	66 ly.ValSerSerThrSerAsnMetHisGlySerLeuLeuGlnGluLysHi 6 :: ::::: :::	
66 345	49 rSerValSerValThrSerProSerGlyValSerSerSerThrSerGlyG 6 ::: :::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: :: ::: ::: ::: :: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::::	
49 295	33 yHisSerSerLeu.ThrAsnSerProLeuAspSerSerCysLys.GluSe 6 : :::::::: ::	63 2 24
33 245	17 GlyHisLysLysLeuLeuGlnLeuLeuThrCysSerSerAspAspArgGl 6 ::: :::::::::::::::::::::::::::::::	61 220
204	::::::::::::::::::::::::::::::::::::::	

1 MetSerGlyLeuGlyGluAsnLeuAspProLeuAlaSer :::: 29 ATGGAGGGCGCGGCGGCGCGACGACAAGAAAAAGATAAGTTCT	alignment_block: US-09-041-994-2 x US-08-480-473B-1 Align seg 1/1 to: US-08-480-473B-1 from: 1 to: 3736	alignment_scores: Quality: 258.00 Length: 915 Quality: 0.604 Gaps: 41 Percent Similarity: 46.667 Percent Identity: 19.781	INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 3736 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: DNA US-08-480-473B-1	NAME: Haile, Lisa A. RECISTRATION NUMBER: 38,347 REFERENCE/DOCKET NUMBER: 07265/053001 TELECOMMUNICATION INFORMATION: TELEPHONE: 619/678-5070 TELEPHONE: 619/678-5070	CURRENT APPLICATION DATA; APPLICATION NUMBER: US/08/480,473B FILING DATE: 06-JUN-1995 CLASSIFICATION: 514 ATTORNEY/ARGENT INFORMATION:	ADABLE FORM: TER Floppy disk IBM PC compatible SYSTEM: PC-DOS/MS-DOS	; CORRESPONDENCE ADDRESS: ; ADDRESSEE: Fish & Richardson P.C. ; STREET: 4225 Executive Square, Suite 1400 ; CTTY: La Jolla ; STATE: CA ; COUNTRY: USA	<pre>seq_documentation_block: ; Sequence 1, Application US/08480473B ; Patent No. 5882914 ; GENERAL INFORMATION: ; APPLICANT: Semenza, Gregg L. ; TITLE OF INVENTION: HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF USE ; NUMBER OF SEQUENCES: 64</pre>	<pre>seq_name: /cgn2_6/ptodata/1/ina/5B_COMB.seq:US-08-480-473B-1</pre>	956 GlySerIleProThrLeuProLeuArgSerAsnSerIleProGly 970 :::	939 lyArgProGlyGlyAspTyrAsnThrSerLeuProArgProAlaLeuGly 955 ::: :::	922 uProAsnSerLysAlaGlyArgMetGluProMetAsnSerAsnSerMetG 939 ::: ::::::: ::::: ::: :::::: 2988 .CCCTCCCGCAGGGTCAGCCGGCTGTCAGAGTCCTAAGGTCTCC 3030	906 AsnArgAsnValThrValThrGlnThrproSerSerGlyAspTrpGlyLe 922 ::: 2955 GCCACACAGTCTACACCTCCGGAACCCCCACGC	2937GGAACCCTGGGCTATGCA 2954

288	.eAspThrAsnSerLeuArgSerSe	67
271 766	nProGluSerPheIleThrArgHis 	261 17
261 716	ValAlaArgArgIleThrThrGlyGluArgThrPheP 	82
244 681	LeuSerGlnProArgAlaMetMetGluGluGlyGluAspLeuGlnSe ::: AAGAAACCACCTATGAC	228 562
227 661	AsnAlaSerProGluMetArgGlnArgTyrGluThrMetGlnCysPhe :::::	211 536
211 635	ArgMetLeuMetLysThrProHisAspIleLeuGluAspI :::::	989
197 585	HisThrPheAsnCys. :: :: :: AATGAAGTGTACCCTAACTAGCCGAGGAAGAACTATGAACATAI	193 536
192 535	ThrAsnGluProGlnArgGlnLysSer	186 180
180 485	luAspArgLysAspPheLeuLysAsnLeuProLysSerThrValAsnG ::::::::::::: :::::::::::::::	L63
163 441	rLysGlnGluAspLeuValAsnThrSerValTyrAsnIleLeuHisGl ::: :::: ::::: AACTCAGTTTGAACTAACTGGACACAGTGTGTTTGATTTTACTCATCC	L47 392
146 391	GluAlaAsnIleValPheValSerGluAsnValThrGlnTyrLeuGln :::::::::: ::: :: ::: :: GATGGTGACATGATTTACATTTCTGATAATGTGAACAAATACATGGGA	L30
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113 291	erThrGlyGlnGlyValIleAspLysA AAAG	97 281
96 280	<pre>GGluGlnGlyLysThrIleSerAsnAspAspAspValGln ::::</pre>	80 237
80 236	roaspLysCysAlaIleLeuLysGluThrValArgGlnIleA :::::::: ::: ::::::::	65 L87
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48 148	SATGATGATGGluGlnGluSerLySTyTleGluGluLeu : ::::: ::: ATCTCGGCGAAGTAAAGAATCTGAAGTTTTTTATGAGCTT	32 99
86		79

562	SerLysV	558
in i	GAACCAAATCCAGAGTCACTGGAACTTTCTTTTACCAT	σ 4
55B	Cordroid verolver and endender Cordroiden Mothern Lothrol	540
4 1	aLeuGlnAlaIleSerGluGlyValGlyThrSerLeuLeuSerThrLeu	52
1429	AAGTAGTGCTGAC	1417
525	rSerGlyAsnThrGlyAsnHisSerPheSerSerSerSerLeuSerA	508
508 1416	IleAlaSerHisGlnPheSerProValAlaGlyValHisSerProMetAl :: :: :: :::	492 1385
Ĺu	ACAGAATATAAATTTGGCAATGTCTCCA	1356
491	leMetIleSerProArgAsnArgGlySerProLys	479
478 1355	ProProHisGlySerProGlyLeuAlaProAsnGlnGln. :::::::: ::: ::::::	466 1306
465 1305	AsnAsnAsnTyrGlyLeuAsnMetSerSer	456 1256
N	-	1218
1217	AACTTAAGAAGGAACCTGATGCTT	1168
39	oSerThrThrGlyGlnMetSerGlyAlaArgTyrGlyGlySerSerAsnI	4 2
422 1167		406 1118
405 1117	SerMetSerPro	402 1068
0		1052
1051	T) DATGDTOMOT A 1 aG 1 (O'ce Aso Corsorva 1 G 1 cG 1 cMot	1051
386	nG1	370
369 1051	rgAsnProValThrAsnAspArgHisGlyPheValSerThrHisPheLeu :::::::: ATAACACCAAGAATTCTCAACCACAGTGCATTGTATGTGTGAATTACGTT	353 1002
353 1001	rLeuAlaAspGlyThrlleValThrAlaGlnThrLysSerLysLeuPheA	336 952
336 951	GlnGluAlaTyrLeuAsnGlyHisAlaGluThrProValTyrArgPheSe ::: :::	320 905
319 904	rgPhePheSerLeuAsnAspGlyGlnSerTrpSerGlnLysArgHisTyr::::::::::::::::::::::::::::::::::::	303 858
303 857	<pre>rMetArgProGlyPheGluAspIleIleArgArgCysIleGlnA :</pre>	288 808

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seq_name: /cgn2_6/ptodata/1/ina/6A_COMB.seq:US-08-915-213-1
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                                                                      2312 GAACAGAATGGAATGGAGCAAAAGACAATTATTTTAATACCCTCT 2356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2012 ACTCAAAGTCGGACAGCCTCACCAAACAGAGCAGGAAAAGGAGTCATAGA 2061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1912 AAAAGACCGTATGGAAGACATTAAAATATTGATTGCATCTCCATCTCCTA 1961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1812 CTCAAAGCACAGTTACAGTATTCCAGCAGACTCAAATACAAGAACCTACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      laGluValAlaLysIleThrAlaGlnAlaThrGly......LysAsp 709
                                                                                                                                                                                                      CAGCTACTACATCACTTTCTTGGAAACGTGTAAAAGGATGCAAATCTAGT 2311
                                                                                                                                                                                                                                                                     spAlaLeuSerLysGluLeuGlnProGlnValGluGlyVal.....
                                                                                                                                                                                                                                                                                                                                         TTTTCAAGCAGTAGGAATTGGAACATTATTACAGCAGCCAGACGATCATG 2261
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                                                                                                                                                                                                                                                                                                                                                                                                        u......ArgTyrLeuLeuAspArgAspAspProSerA 749
                                                                                                                                  ...AspAsnLysMetSerGlnCysThrSerSerThrIleProSer 776
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TOPOLOGY: 1:
; MOLECULE TYPE:
US-08-915-213-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_scores:
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Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: US-08-915-213-1 from: 1
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APPLICANT: Semenza, Gregg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915
EILING DATE: 20-AUG-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/480
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REGISTRATION NUMBER: 38,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                     149
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187 TCTTGATAAGGCCTCTGTGATGAGGCTTACCATCAGCTATTTGCGTGTGA
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                                                                                                                                                                                                                                                                                                                                                                                             32 erGlyGluLysArgArgGluGlnGluSerLysTyrIleGluGluLeu 48
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                                                                            65 sProAspLysCysAlaIleLeuLysGluThrValArg.....GlnIleA 80
                                                                                                                                                                                                                                         49 AlaGluLeuIleSerAlaAsnLeuSerAspIleAspAsnPheAsnValLy 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79 TCGAAAAGAAAAG......TCTCGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
                                                                                                                                                                                                                                                                                                                             ATGCAGCCAGATCTCGGCGAAGTAAAGAATCTGAAGTTTTTTATGAGCTT 148
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                                                                                                                                                            .CAGTTGCCACTTCCACATAATGTGAGTTCGCA 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64
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Percent Identity: 19.781
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rgAsnProValThrAsnAspArgHisGlyPheValSerThrHisPheLeu 3	TGCCAAAAGAGGTGGATATGTCTGGGTTGAAACTCAAGCAACTGTCATAT 1	lyThrIleValThrAlaGlnThrLysSerLysLeuPheA 3	GACAGTACAGGATGCT 9	luAlaTyrLeuAsnGlyHisAlaGluThrProValTyrArgPheSe 3	erGlnLysArgHisTyr ::::: CAAAACTCATCAT	AGCCAGAAGAACTTTTAGGCCGCTCAATTTATG	ArgCysIleGlnA :	SCCTSGATATGAAATTTTCTTATTGTGATGAAAGAATTAC	LeuSerGlyLysValValAsnIleAspThrAsnSerLeuArqSerSe	elleThrArgHis 2 :::::: CCTCAGTCGACAC 7	CTGCTTGGTGCTGATTTGTGAACCCATTCCTCACC 7	rCysMetIleCysValAlaArgArgIleThrThrGlyGluArgThrPheP 2	TATAAGAAACCACCTATGAC 6	AlaLeuSerGlnProArgAlaMetMetGluGluGlyGluAspLeuGlnSe 2	TGGG		TGCAACATGGAAGGTATTGCACTGCACAGGCCACATTCACGTATATGATA 6	ArgMetLeuMetLvsThrProHisAspIleLeuGluAspI	CTATGAACATAAAGTC	HisThrPheAsnCvs 1	GCGAAGCTTTTTCTC	luProGlnArgGlnLysSer		AGTTTGAACTAACTGGACACAGTGTGTTTTGATTTTTACTCATCC 4	TyrLysGlnGluAspLeuValAsnThrSerValTyrAsnIleLeuHisGl 1	GTGACATGATTTACATTTCTGATAATGTGAACAAATACATGGGA 3	luAlaAsnIleValPheValSerGluAsnValThrGlnTyrLeuGln	TGCTTTTATTTGAAAGCCTTGGATGGTTTTGTTATGGTTCTCACAG 3	GlyProLeuLeuClnAlaLeuAspGlyPheLeuPheValValAsnA	AAAGCACAGAT	Le	
69	001	53	51	36	319 904	857	303	807	288	71	716	261	681	244	661	27	35	211	585	197	35	192	180 485	41	163	191	146	41	130	291	113	280

626	rgGlyProLeuGluSerLysGlyHisLysLysLeuLeuGlnLeuLeuThr	610
1669	TGAA	1651
610	uSerAspLysGluSerLysGluSerSerValGluGlyAlaGluAsnGlnA	593
593 1650	GlnasnProValGluSerSerMetCysGlnSerAsnSerArgaspHisLe :::::: ::::::	577 1601
576 1600	2 alserAsnGlnAspSerLysSerProLeuGlyPheTyrCysAsp ::: :: AAAGTTCACCTGAGCCTAATAGTCCCAGTGAATATTGTTTTTATGTGGAT	562 1551
562 1550	8 nProSerLysV : : GCCCCAGATTCAGGATCAGACACCTAGTCCTTCCGATGGAAGCACTAGAC	558 1501
558 1500	2 SerSerProGlyProLysLeuAspAsnSerProAsnMetAsnIleThrGl ::: :: ::: ::	542 1463
541 1462	laLeuGlnAlaIleSerG ::::::: CCTGCACTCAATC	525 1430
1429	8 aSerSerGlyAsnThrGlyAsnHisserPheSerSerSerSerLeuSerA ::::: 7 AAGTAGTGCTGAC	1417
4 0	THEATASETHISGINFRESETFTOWALA HAGITYBIHLISSETFTOWALA : : : : : : : : : : : : : : : : :	1385
, ω ω	TACAGAATATAAATTTGGCAATGTCTCCA	5 7
u 7	ProProHisGlySerProGlyLeuAlaProAsnGlnG	466 1306
465 1305	6 ASNASNASNTYYGLYLEUASNMEtSerSer6 ::: ::::: ::::: 6 TCTTTAGATTTTGGCAGCAACGACACAGAAACTGATGACCAGCAACTTGA	450 1250
455 1255	9 leAlaSerLeuThrProGlyProGlyMetGlnSerProSerSerTyrGln ::::: ::: ::: 8 TAACTTTGCTGGCCCCAGCCGCTGGAGACACAATCATA	439 1218
	2 oSerThrThrGlyGlnMetSerGlyAlaArgTyrGlyGlySerSerAsnI ::: ::::::: 8 AGAAGATACAAGTAGCCTCTTTGACAAACTTAAGAAGGAACCTGATGCTT	422 1168
422 1167	6 AsnGlnGlyLeuGlnMetProSerSerArgAlaTyrGlyLeuAlaAspPr ::::::::::::::::::::::::::::::::::::	406 1118
405 1117	2SerMetSerPro :::::: ::::::: ::::::::::::::::::	1068
1067	A T T COLT A L T C L C C C C C C C C C C C C C C C C	1052
1051		1051
386	0 GlnArgGluGlnAsnGlyTyrArgProAsnProAsnProValGlyGlnGl	37(
1051	::::::::::::::::::::::::::::::::::	1002

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seq_documentation_block:
   Sequence 1, Application US/09148547
   Patent No. 6124131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: /cgn2_6/ptodata/1/ina/6B_COMB.seq:US-09-148-547-1
                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Semenza, Gregg L.
TITLE OF INVENTION: Hypoxia Inducible Factor-1 and Methods of Use
FILE REFERENCE: 07265/151001
CURRENT APPLICATION NUMBER: US/09/148,547
CURRENT FILING DATE: 1998-08-25
                                                                              NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTIN VER. 2.0
SEQ ID NO 1
LENGTH: 3736
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                                                      TYPE: DNA
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                  ORGANISM: Homo sapiens
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FEATURE:
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alignment_block:
US-09-041-994-2 x US-09-148-547-1
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636 CCAACAGTAACCAACCT..
                                               211 leAsnAlaSerProGluMetArgGlnArgTyrGluThrMetGlnCysPhe 227
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                                                                                                                                                                                                                                                                                                                                                                                                      442 ATGTGACCATGAGGAAATGAGAGAAATGCTTACACAGA.....AATG 485
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15 rArgLysArgLysLeuProCysAspThrProGlyGlnGlyLeuThrCysS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29 ATGGAGGCGCCGCGCGCGCGAACGAAGAAAAAGATAAGTTCTGAACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MetSerGlyLeuGlyGluAsnLeuAsp.....ProLeuAlaSerAspSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGAAACTTCTGGATGCTGGT...GATTTGGATATTGAAGATGACATG... 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sProAspLysCysAlaIleLeuLysGluThrValArg.....GlnIleA 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          erGlyGluLysArgArgGluGlnGluSerLysTyrIleGluGluLeu
                                                                                                 TGCAACATGGAAGGTATTGCACTGCACAGGCCACATTCACGTATATGATA 635
                                                                                                                                                                                                     AGAATGAAGTGTACCCTAACTAGCCGAGGAAGAACTATGAACATAAAGTC
                                                                                                                                                                                                                                                                                                       GCCTTGTGAAAAAGGGTAAAGAACAAAACACACAGCGAAGCTTTTTTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                     uGluAspArgLysAspPheLeuLysAsnLeuProLysSerThrValAsnG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTAACTCAGTTTGAACTAACTGGACACAGTGTGTTTTGATTTTACTCATCC 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rgGluAlaAsnIleValPheValSerGluAsnValThrGlnTyrLeuGln 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  uGlyProLeuLeuGlnAlaLeuAspGlyPheLeuPheValValAsnA 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LysalaaspValSerSerThrGlyGlnGlyValIleaspLysaspSerLe 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rgGlnIleLysGluGlnGlyLysThrIleSerAsnAspAspAspValGln 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCTCAT.....CAGTTGCCACTTCCACATAATGTGAGTTCGCA 186
                                                                                                                                              .....ArgMetLeuMetLysThrProH1sAspIleLeuGluAspI 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ratio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-148-547-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           258.00
0.604
46.667
                                                                                                                                                                                                                                                  ..........HisThrPheAsnCys..... 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps: 41
Percent Identity: 19.781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .....AAAGCACAGAT 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .....TCTCGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <u>د</u>
CAGTGTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   341
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ن ن	GAATATAAATTTGGCAATGTCTCCA	Ċπ
491	AsnIleMetIleSerProArgAs	479
478 1355	ProProHisGlySerProGlyLeuAlaProAsnGlnGln.	466 1306
465 1305	AsnAsnAsnTyrGlyLeuAsnMetSerSer	456 1256
455 1255	leAlaSerLeuThrProGlyProGlyMetGlnSerProSerSerTyrGln :::: :::	439 1218
439 1217	rgTyrGlyGlySerSerAsnI ::: TAAGAAGGAACCTGATGCTT	422 1168
422 1167	AsnGlnGlyLeuGlnMetProSerSerArgAlaTyrGlyLeuAlaAspPr ::::::::::::::::::::::::::::::::::::	406 1118
405 1117	SerMet ::: CCCTTCAACAAACAGAATGTGTCCTT	402 1068
1067	Ometatactycysh	1052
1051	1123779137917917917917917917917917917917917917917	n un
386	${\tt GlnArgGluGlnAsnGlyTyrArgProAsnProAsnProValGlyGlnGl}$	370
369 1051	rgAsnProValThrAsnAspArgHisGlyPheValSerThrHisPheLeu :::::::: ATAACACCAAGAATTCTCAACCACAGTGCATTGTATGTGTGAATTACGTT	353 1002
353 1001	rLeuAlaAspGlyThrIleValThrAlaGlnThrLysSerLysLeuPheA	336 952
336 951	GlnGluAlaTyrLeuAsnGlyHisAlaGluThrProValTyrArgPheSe ::: ::: :: ::::	320 905
319 904	rgPhePheSerLeuAsnAspGlyGlnSerTrpSerGlnLysArgHisTyr::::::::::::::::::::::::::::::::::::	303 858
303 857	rgProGlyPheGluAspIleIleArgArgCysIleGlnA ::: :::::: : GATGGGATATGAGCCAGAAGAACTTTTAGGCCGCTCAATTTATG	288 808
288 807	alAsnIleAspThrAsnSerLeuArgSerSe 	272 767
271 766	AsnProGluSerPheIleThrArgHis 	261 717
261 716	rgThrPheP CCTCACC	244 682
244 681	AlaLeuSerGlnProArgAlaMetMetGluGluGlyGluAspLeuGlnSe ::: :::: TATAAGAAACCACCTATGAC	228 662

738	LysLysGluAsnAsnAlaLeuLe	731
2161	TACTA	2112
730	lnLeuSerProLys	720
2111	ACAGACAGAAAAATCTCATCCAAGAAGCCCCTAACGTGTTATCTGTCGCTT	2062
719		719
719 2061	ThrSerSerIleThrSerCysGlyAspGly ::: ::: ::: ACTCAAAGTCGGACAGCCTCACCAAACAGAGCAGGAAAAGGAGTCATAGA	710 2012
709 2011	laGluValAlaLysIleThrAlaGlnAlaThrGlyLysAsp :::::::	696 1962
696 1961	uLysHisArgIleLeuHisLysLeuLeuGlnAsnGlyAsnSerProA 	680 1912
1911 1911	SerGlyGlyValSerSerThrSerAsnMetH1sGlySerLeuLeuGlnGl::::::::::::::::::::::::::::::::::	664 1862
663 1861	ysGluSerSerValSerValThrSerProSerGlyValSerSerSerThr::: ::: ::: :::	647 1812
647 1811	uThrAsnSerProLeuAspSerSerCysL : : :	637 1768
637 1767	CysSerSerAspAspArgGlyHisSerSerLe	627 1718
626 1717	rgGlyProLeuGluSerLysGlyHisLysLysLeuLeuGlnLeuLeuThr ::: :::: :::	610 1670
610 1669	uSerAspLysGluSerLysGluSerSerValGluGlyAlaGluAsnGlnA :: ::: TGAAGACACAGAAGCAAAG	593 1651
593 1650	GlnAsnProValGluSerSerMetCysGlnSerAsnSerArgAspHisLe ::::: ::::: AGTGATATGGTCAATGAATTCAAGTTGGAATTGGTAGAAAAACTTTTTGC	577 1601
576 1600	alSerAsnGlnAspSerLysSerProLeuGlyPheTyrCysAsp :: :: :: AAAGTTCACCTGAGCCTAATAGTCCCAGTGAATATTGTTTTTATGTGGGAT	562 1551
562 1550	nProSerLysV 	558 1501
558 1500	SerSerProGlyProLysLeuAspAsnSerProAsnMetAsnIleThrGl ::: ::: :: :: :GAACCAAATCCAGAGTCACTGGAACTTTCTTTTACCAT	542 1463
541 1462	laLeuGlnAlaIleSerGluGlyValGlyThrSerLeuLeuSerThrLeu	525 1430
525 1429	rGlyAsnH1sSerPheSerSerSerSerLeuSerA	508 1417
508 1416	IleAlaSerHisGlnPheSerProValAlaGlyValHisSerProMetAl	492 1385

32	15 rArgLysArgLysLeuProCysAspThrProGlyGlnGlyLeuThrCysS: ::: 79 TCGAAAAGAAAAGTCTCGAG
15 78	1 MetSerGlyLeuGlyGluAsnLeuAspProLeuAlaSerAspSe
	lign seg 1/1 to: PCT-US96-10251-1 from: 1 to: 3736
	1gnment_block: S-09-041-994-2 x PCT-US96-10251-1
	<pre>ignment_scores: Quality: 258.00</pre>
	TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: DNA T-US96-10251-1
	ELEPHONE: 619/678-5ELEFAX: 619/678-5MATION FOR SEQ ID UENCE CHARACTERIST
	ATTORNEY/AGENT INFORMATION: NAME: Haile, Lisa A. REGISTRATION NUMBER: 38,347 REFERENCE/DOCKET NUMBER: 07265/053WO1 TELECOMMUNICATION INFORMATION:
	APPLIC FILING
	TYPE: F1 ER: IBM P ING SYSTEM RE: Paten
	STATE: CA COUNTRY: USA CIP: 92037 COMPUTER READABLE FORM:
	ADDRESSEE: Fish & Richardson P.C. STREET: 4225 Executive Square, Suite 1400 CITY: La Jolla
cine HOD OF USE	INFORMATION: ANT: The Johns OF INVENTION: OF SEQUENCES:
	<pre>q_documentation_block: Sequence 1, Application PC/TUS9610251</pre>
1-1	q_name: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:PCT-US96-1025
	763AspAsnLysMetSerGlnCysThrSerSerThrIleProSer 776 ::: :::
762 2311	749 sphlaleuSerLysGluLeuGlnProGlnValGluGlyVal
749 2261	738 uArgTyrLeuLeuAspArgAspAspProSerA
2211	2162 GCTTTGCAGAATGCTCAGAGAAAGCGAAAAATGGAACATGATGGTTCACT

303 857	288 rmetArgProGlyPheGluAspIleIleArgArgCysIleGlnA : ::: : 808 CGAATTGATGGGATATGAGCCAGAAGAACTTTTAGGCCGCTCAATTTATG
288 807	272 AspLeuSerGlyLysValValAsnIleAspThrAsnSerLeuArgSerSe::: ::: ::: :: ::: :: :: :: :: :: :: :: :: ::
271 766	261 roSerasnProGluSerPheIleThrArgHis
261 716	laArgArgIleThrThrGlyG ::::: GTGAACCCATT
244 681	Alametmet
227 661	211 leAsnAlaSerProGluMetArgGlnArgTyrGluThrMetGlnCysPhe
211 635	198ArgMetLeuMetLysThrProHisAspIleLeuGluAspI
197 585	193HisThrPheAsnCys ::: ::: ::: : 536 AGAATGAAGTGTACCCTAACTAGCCGAGGAAGAACTATGAACATAAAGTC
192 535	180 lyValSerTrpThrAsnGluProGlnArgGlnLysSer
180 485	163 uGluAspargLysAspPheLeuLysAsnLeuProLysSerThrValAsnG
163 441	147 TyrLysGlnGluAspLeuValAsnThrSerValTyrAsnIleLeuHisGl
146 391	130 rgGluAlaAsnIleValPheValSerGluAsnValThrGlnTyrLeuGln ::::::::::::::::::::::: ::: :::
130 341	.euLeuLeuGlnAlaLeuAspGlyPheLe :: ::: TTTATTTGAAAGCCTTGGATGGTTTTGT
113 291	rGlyGlnGlyValI
96 280	80 rgGlnIleLysGluGlnGlyLysThrIleSerAsnAspAspAspAspValGln ::::: ::
80 236	65 sProAspLysGysalaTleLeuLysGluThrValArgGlnTleA ::::::::::::: ::::::::::: 187 TCTTGATAAGGCCTCTGTGATGAGGCTTACCATCAGCTATTTGCGTGTGA
65 186	lese
48 148	32 erGlyGluLysArgArgArgGluGlnGluSerLysTyrIleGluGluLeu ::::: :::: ::: 99 ATGCAGCCAGATCTCGGCGAAGTAAAGAATCTGAAGTTTTTATGAGCTT

7 6	a corporation to the corporation to the contraction of the corporation to the corporation	ر در در
1550	GCCCCAGATTCAGGATCAGACACCTAGTCCTTCCGATGGAAGCACTAGAC	.501
562	ProSerLy	558
558 1500	SerSerProGlyProLysLeuAspAsnSerProAsnMetAsnIleThrGl ::: ::: :: :: :: :: ::	542 463
541 1462	laLeuGlnAlaIleSerGluGlyValGlyThrSerLeuLeuSerThrLeu	525 [430
1429	TAGTGC	1417
525	. ia	508
508 1416	IlealaSerHisGlnPheSerProValAlaGlyValHisSerProMetAl :: :: :: ::	492 1385
1384	CAGAATATAAATTTGGCAATGTCTCCA	1356
491	IleMetIleSerPr	479
478 1355	ProProHisGlySerProGlyLeuAlaProAsnGlnGln. ::::::::	466 1306
465 1305	ASnAsnAsnTyrGlyLeuAsnMetSerSer	456 1256
455 1255	leAlaSerLeuThrProGlyProGlyMetGlnSerProSerSerTyrGln:::: ::: ::::	439 1218
439 1217	OSETThTThTG1yG1nMetSerG1yA1aArgTyrG1yG1ySerSerAsnI ::: :::::::: AGAAGATACAAGTAGCCTCTTTGACAAACTTAAGAAGGAACCTGATGCTT	422 1168
422 1167	AsnGlnGlyLeuGlnMetProSerSerArgAlaTyrGlyLeuAlaAspPr ::::::::::::::::::::::::::::::::::::	406 1118
405 1117	AGCACGACTTGATTTTCTCCCTTCAACAAACAGAATGTGTCCTTAAACCG	1068
1067	::: ::: ::: ::: ::: ::: :::	1052
401	.leArgProProMetAlaGlyCysAsnSerSerValGlyGlyMet	æ
0		σ.
388 TCOT	AACACCAAGAAIICICAACCACAGIGCAIIGIAIGIGIGIG	v
0.0	gAsnProValThrAsnAspArgHisGlyPheValSerThrHis :::::: ::: :::: ::::::	353
353	rLeuAlaAspGlyThrIleValThrAlaGlnThrLysSerLysLeuPheA	336 952
336 951	GINGIUAIaTyrLeuAsnGlyHisAlaGluThrProValTyrArgPheSe ::: ::	905
904		858
319	rgPhePheSerLeuAsnAspGlyGlnSerTrpSerGlnLysArgHisTyr	303

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alignment_block:
us-09-041-994-2 x us-08-194-468-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; NAME/KEY:
; LOCATION:
US-08-194-468-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: US-08-194-468-1 from: 1 to: 7326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/194,468
FILING DATE: 10-FEB-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Reiter, Stephen E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P41 9672
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (619)-546-9392
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 7326 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                    5644 AGTTTGCCTTCTCCTACCTCAGCACCACCCGGGACTCCTACACAGCAG. 5691
                                                                                                                                                                                                                                                      5692 .....CCCAGCACACCCCAAACACCACAGCCCCAGCCCAGCCTC 5731
5769 TAAT.....GTAGCCCGGACTCAGCCCCCAACAATAGTGTCTGCTGGGA 5812
                                                                                                                                                                                                          890 rgMetMetAspSerGlnGluAsnTyrGlySerSerMetGlyGlyProAsn 906
                       907 ArgAsnValThrValThrGlnThrProSerSerGlyAspTrpGlyLeuPr 923
                                                                                                                                                                                                                                                                              873 eSerAlaPheProMetLeuProLysGlnProMetLeuGlyGlyAsnProA 890
                                                                                                                                                                                                                                                                                                                                                              857 SerLeuAspSerProValSerValGlySerSerProProValLysAsnI1 873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
STREET: 444 South Flower Street, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: MODITMINY, MATC R.
TITLE OF INVENTION: ASSAYS FOR THE IDENTIFICATION OF
TITLE OF INVENTION: COMPOUNDS WHICH INHIBIT ACTIVATION OF CAMP AND MITOGEN
TITLE OF INVENTION: RESPONSIVE GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (619)-546-4737
(619)-546-9392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NO
                                                                                                                                                          DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           254.50
0.887
48.562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length: 591
Gaps: 27
Percent Identity: 24.873
                                                                                  .GGCTTCCC
                                                                                  5768
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1210	etGluAsnProThrAlaGlvGlvAlaAlaValMetArgProMetMet	1195
1195 6646	UGlnGlyGlnGlnPheLeuAsnGlnSerArgGlnAlaLeuGluLeuLysM 	1178 6597
9	ThrProLysGlnLeuArgMetGlnLeuGlnGlnArgLe ::: ::: ::: aTGACAAACATGAATCCACAGTACCGAGAAATGGTGAGGAGACAGCTGCT	
	isProArgAlaAsnIleMetArgProArgThrAsn :: ::::	1154 6497
1154 6496	nMetAsnGlnGlnGlyAsnPheProLeuGln	1141 6447
1141 6446	GlyPheHisLeuGlnGlyGlnSerProSerPheAsnSerMetMetAsnGl ::: ::: ::::: ::: ::: GCATGCACCAGCAGCCTAGTTTGCAAAACCTGAACGCAATGCAAGCTGG	1125 6397
112 4 6396	ly	1112 6353
1112 6352	eGlnGlyGlnGluAlaAlaValMetMetAspGlnLysAlaGlyLeuTyrG 	1095 6303
1095 6302	ProGluLeuValAsnGlnGlyGlnAlaLeuGluProLysGlnAspAlaPh ::: ::: CCACAGCTAATG	1079 6283
1078 6282	snThrAspAlaThrGlyLeuGluGluIleAspArgAlaLeuGlyIle ::::::	1063 6233
1063 6232	uArgālaLeuLeuAspGlnLeuHisThrLeuLeuSerA : :: GAGCATCTCGCCAAGTGCCCTGCAAGACCTGCTACGGACCCTAAAGTCAC	1050 6183
1050 6182	LeuAspAspLeuValGlyProProSerAsnLeuGluGlyGlnSerAspGl::: ::: :::: ::::::::::	103 4 6133
1033 6132	etGluGlnValSerHisGlyThrGlnAsnArgProLeuLeuArgAsnSer:::: ::: ::::	1017 6086
1017 6085	nAlaAlaAlaSerAsnGlnLeuGlySerTrpProAspGlyMetLeuSerM ::: :: ::: :::: ::: :: :: :: ::	1000
1000	ProTyrGlyGl :::	993 5986
992 5985	MetargProGlyGluIleProMetGly	984 5936
983 5935	OValLeuGlnGlnGlnGlnMetLeuGln ::: :::: AATTGAACGTGAGGCCCAGCAGCAGCAGCACCTATACCGAGCAAACATCA	973 5886
973 5885	SerIleProThrLeuProLeuArgSerAsnSerIleProGlyAlaArgPr:::	957 5851
956 5850	rgProGlyGlyAspTyrAsnThrSerLeuProArgProAlaLeuGlyGly :::	940 5813

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GENERAL INFORMATION:
APPLICANT: MONTHIN, MARC R.
TITLE OF INVENTION: Methods for Treating Diabetes Mellitus
FILE REFERENCE: SALK1650-1
CURRENT APPLICATION NUMBER: US/08/961,739A
CURRENT FILING DATE: 1997-10-31
EARLIER APPLICATION NUMBER: US 194,468
EEARLIER FILING DATE: 1994-02-10
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 7326
TYPE: DNA
ORGANISM: Mus
FEARIFEE.
                                                                                                                                                                                                                                                                                                                                                                                                       seq_documentation_block:
; Sequence 1, Application US/08961739A
; Patent No. 6063583
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FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(7326)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1360 nLeuAlaArgAsnSerSerPheSerGlnGlnPheAlaHisGlnGlyA 1377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7047
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                                                   GAGCATCTCGCCAAGTGCCCTGCAAGACCTGCTACGGACCCTAAAGTCAC
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; FEATURE:
; NAME/KEY:
; LOCATION:
US-08-045-806-3
                                                                                               alignment_block:
                                                                                                                                                                                        alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: /cgn2_6/ptodata/1/ina/5A_COMB.seq:US-08-045-806-3
                                                                                                                                  Percent Similarity:
                                     Align seg 1/1
                                                                           US-09-041-994-2 x US-08-045-806-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/08045806 Patent No. 5378822
                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (312)-456-77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1360 nLeuAlaArgAsnSerSerPheSerGlnGlnPheAlaHisGlnGlyA 1377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1344 AlaAlaSerIleTyrGlnSerSerGluMetLysGlyTrpProSerGlyAs 1360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1377 snProAlaValTyrSerMetVal 1384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7085 CGTCACCACGGATACAACCCCAGCCTTCACCACCACCATGTTTCACCCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/01
FILING DATE: 19930408
FILING DATE: 19930408
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Fentress, Susan B.
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 5261 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Dolwick, Kristin Marie
APPLICANT: Poland, Alan
TITLE OF INVENTION: Ah Receptor cDNA and Method of
TITLE OF INVENTION: Determining Human Risks To Envi
                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Tilton, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
15 SerArgLysArgLysLeuProCysAsp.....
                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
TOPOLOGY: un
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Fentress, Susan B. REGISTRATION NUMBER: 31,327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACT.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCCTGAACAGAGTGCAATGCTC
                                                                                                                                                  Quality:
Ratio:
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                                     to: US-08-045-806-3
                                                                                                                                                                                                                                                                                                                                                                                                  5261 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Tilton, Fallon, Lungmus & Chestnut 100 South Wacker Drive, Suite 960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
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                                                                                                                                                                                                                                                                   CDS
383..2927
                                                                                                                                                                                                                                                                                                                                              unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (312)-456-8000
                                                                                                                                252.00
0.545
43.958
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                                                                                                                                Percent Identity:
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                                       from:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .GGAACCCCTCACCCTGG
                                     to:
 ....ThrProGl
                                                                                                                                    19.696
                                       5261
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   26
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416		65
26 466	yGlnGlyLeuThrCysSerGlyGluLysArgArgArgGluGlnGluSerL 4 :::: ::: :::: :::: ::::::::::::::::	15
43 516	ysTyrIleGluGluLeuAlaGluLeuIleSerAlaAsnLeuSerAspIle 5 :::::::::: ::: CAGAGTTGGACCGTTTGGCTAGCCTGCTGCTTTCCCACAAGATGTT 5	62
60 563	AspasnPheAsnValLysProAspLysCysAlaIleLeuLysGluThrVa 7	6
76 604	O - H	553
86 654	lyLysThrIleSerAsnAspAspAspValGlnLysAlaAspValSerSer 1 ::::: ::: ::: CTACTGAAAGAAACGGAGGCCAGGATAACTGTAGAGCAGCAAATTTCAGA 7	02
103 704	ThrGlyGlnGlyValIleAspLySAspSerLeuGlyProLeuLeuLeuGl 1	.19
119 742	H — 0	.36
136 792	heValSerGluAsnValThrGlnTyrLeuGlnTyrLysGlnGluAspLeu 1:::: ::: ::: ::: ATGCTTCTTCTACTATACAAGATTATCTAGGGTTTCAGCAGTCTGATGTC 8	152 841
153 842	ValasnThrSerValTyrAsnIleLeuHisGluGluAspArgLysAspPh 1 :::::	.69 191
	eLeuLysAsnLeuProLysSerThrValAsnGlyValSerTrpThrAsnG :	186
892		192
186 893	luProGlnArgGlnLysSerHisThrPheAsnCysArgMetLcuMetLys 2	202 919
203 920	ThrProHisaspIleLeuGluAspIleAsnAlaSerProGluMetArgGl 2 :::	19
219 967	nargTyrGluThrMetGlnCysPheAlaLeuSerGlnProArgAlaMetM 2 ::: ::: ::: ::: TCTCCCCCAGACAGTAGTCTGTTATAACCCAGACCAGA	236
236 008	etGluGluGlyGluAspLeuGlnSerCysMetIleCysValAlaArg 2 ::::: ::: ::: CTCCAGAAAACTCTCCTTTAATGGAGAGGTGCTTCATATGTCGTCTAAGG 1	.057
252 058	ArgIleThrThrGlyGluargThrPhe	107
260		60
108	GTTAAAGTATCTTCATGGACAGAAAAAGGAAAGGGGAAAGATGGATCAATAC 1	157
261 158	TTOO ACCTO A	207
266	Ser	71

1208	TCCATACTTGAAATCCGGACCAAAAATTTTATCTTTAGAACCAAACACAA	1257
272	AspLeuSerGlyLysValValAsnI	280
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280	uAspIle	296
1308	GATATACTGAAGCAGAGCTGTGCACGAGAGGCTCAGGTTATCAGTTTATT	1357
297	:	298
1358	CAGCTGATATGCTTATTGTGCCGAGTCCCATATCCGAATGATTAA	1407
299		310
1408	GAAAGTGGCATGATAGTTTTCCGGCTTCTTACAAAAAACAACC	1457
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327	laGluThrProValTyrArgPheSerLeuAlaAspGlyThrIleVa	343
1505	AGACCAGATTATATCATTGT	1524
343 1525	SSerLysLeuPheArgAsnProValThrAsnAspA ::::: ::: :::: CAGAGACCACTAACAGATGAGG	360 1550
360	sGlvPheValSerThrHisPheLeuGlnArgGluGlnAsnGlvTvr	76
1551	GGAACAGAGCATTTACGAAAACGAAATACGAAG	1585
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1715	ATGAT	1764
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451	<pre>:erSerTyrGlnAsnAsnAsnTyrGlyLeuAsnMetSerSerProPro :: ::::: </pre>	467
1815	CCTTTTGAAAACAACTTTTTCAACGAATCTATGAATGAAT	1864
468	SerProGlyLeuAlaProAsnGlnGlnAsnIleMetIleSerPr	484
1865		1888
484	AlaSerHisGlnPheSerProVálA	501
1889	ATACTATCCTGAAACATGAG	1918
501	etAlaSerSerGlyAsnThrGlyAsnHisSer	517
1919	CAAATTGACCAGCCTCAGGATGTGAACTCATTTGCTGGAGGTCACCCA	1966
518	erSerSerLeuSerAlaLeuGlnAlalleSerGluGl	w
1967	GGCTCTTTCAAGATAGTAAAAACAGTGACTTGTACAGCATAATGAAAAA	2016

532	yValGlyThrSerLeuLeuSerThrLeuSerSerProGlyProLysLeuA	549
2017	CCTAGGCATTGATTTT	2032
5.4	pAsnSe	65
2000	- GAAGACATCAGACATGCAGAATGAAAAATTTTTT	20/4
2075	ASPSELLYSSELFICHEUSTYFHETYFCYSASPGINASHFIOVALGIUSE	2098
58	${\tt SerMetCysGlnSerAsnSerArgAsp\ldots}.$	98
2099	AGAGACATTGACTTAACGGAT	2119
598	${\tt erLysGluSerSerValGluGlyAlaGluAsnGlnArgGlyProLeuGlu}$	614
2119		2119
<u>5</u> 19	LysLeuLeuGlnLeuLeuThrCysSerS	631
2120	::::::::::::::::::::::::::::::::::::::	2143
631	AsnSerPr	641
2144	Αī	2180
642	ersercy	651
2181	CAAC	2220
652	rVa ∶	668
2221	GGAACACCTACATCTAGAACAGCAACAGCAACATCACCAAAAAGC	2270
668 2271	TSGTThrSerAsnMetHisGlySerLeuLeuGlnGlu, LysHisArgIle	684 2320
685	sLeuLeuGlnAsnGl	701
2321	GTTAATGGCATGTTTGAAAATTGGAACTCTAACCAAATCGTGCCTTTCAA	2370
701	erSerIleT	718
2371	AACAATATAA	2411
718	'n	34
1 6	SORI CROI CRAORO	1 40
7456	ASHATALEULeuArgTyrLeuLeuAspArgAspAspProSerAs ::::::::::::::::::::::::::::::::::::	749
749	AlaLeuSerLysGluLeuGlnProGlnValGluGlyValAspAsnLys	766
2501	:::	2513
766	ThrSerSerThrIlePro	œ
7	oLvsIleLvsThrGluThrSerGluGluGlvSerGlvAspLeu&	799
2564	:::::: CTTCTAGTTTAGAA	2590
799	nLeuAspAlaIleLeuGlyAspLeuThrSerSerAspPheTyrAsnA	815
2591	GATTTTGTCACTTGTT	2606

NUMBER OF SEQUENCES: 36 CORRESPONDENCE ADDRESS: ADDRESSEE: Tilton, Fallon, Lungmus & Chestnut STREET: 100 South Wacker Drive, Suite 960 CITY: Chicago STATE: Illinois COUNTRY: USA ZIT: 60606-4002 COMPUTER: EADABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION NUMBER: US/08/366,051B FILING DATE: APPLICATION NUMBER: US/08/366,051B FILING DATE: APPLICATION NUMBER: 16,926 REGISTRATION NUMBER: 16,926 REFERENCE/DOCKET NUMBER: NU-9207-CIP TELEPHONE: (312)-456-8000 TELEPHONE: (312)-456-8000 TELEFAX: (312)-456-8776 INFORMATION FOR SEQ ID NO: 3:	<pre>seq_name: /cgn2_6/ptodata/1/ina/5A_COMB.seq:US-08-366-051B-3 seq_documentation_block: sequence 3, Application US/08366051B Patent No. 5650283 GENERAL INFORMATION: APPLICANT: Bradfield, Christopher A. APPLICANT: Dolwick, Kristin M. APPLICANT: Carver, Lucy A. TITLE OF INVENTION: Engineered Cells for Detecting Agonists to TITLE OF INVENTION: Receptor</pre>	932 PrometAsnSerAsnSerMetGlyArgProGlyGlyAspTyrAsnThrSe 948 :::::	898 rGlySerSerMetGlyGlyProAsnArgAsnValThrValThrGlnThrP 915	848 eArgProProTyrAsnArgAlaValSerLeuAspSerProValSerValG 865 ::::::::::::::::::::::::::::::::::::	815 snSepileSerSerAsnGlySerHisLeuGlyThrLysGlnGlnValPhe 831 :::::: 2607 TACAACTTCCTGAAAACCAAAAGCAT
	the Ah				

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; NAME/KEY:
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US-08-366-051B-3
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US-09-041-994-2 x US-08-366-051B-3
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Ratio: 0.545
Percent Similarity: 43.958
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                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 5261 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
                                    203 ThrProHisAspIleLeuGluAspIleAsnAlaSerProGluMetArgGl 219
                                                                                   893
                                                                                                          186 luProGlnArgGlnLysSerHisThrPheAsnCysArgMetLeuMetLys
                                                                                                                                                                                                         169 eLeuLysAsnLeuProLysSerThrValAsnGlyValSerTrpThrAsnG 186
                                                                                                                                                                                                                                                                                                                                                      136 heValSerGluAsnValThrGlnTyrLeuGlnTyrLysGlnGluAspLeu 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               103 ThrGlyGlnGlyValIleAspLysAspSerLeuGlyProLeuLeuCel 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          563 ATTAAT.....AAGTTGGACAAACTTTCAGTTCTTAGGCTCAGCGT 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        466 TGAAGGAATCAAGTCAAATCCTTCCAAGCGGCATAGAGACCGACTTAATA 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: CDNA
920 ...CCTTCTCAGTGTACAGAGTCTGGACAAGGAATTGAAGAAGCCACTGG 966
                                                                                                                                                                    892 T.....
                                                                                                                                                                                                                                                                                                                                792 ATGCTTCTTCTACTATACAAGATTATCTAGGGTTTCAGCAGTCTGATGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               704 GAAGGCCTGAACTTACAAGAA......GGAGAATTCTTATTACA 741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                654 CTACTGAAAGAAACGGAGGCCAGGATAACTGTAGAGCAGCAAATTTCAGA 703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             604 CAGTTACCTGAGAGCCAAGAGCTTCTTTGATGTTGCATTAAAATCCTCCC 653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            416 AGTCGCAAGCGGCGGAAGCCGGTGCAGAAAACAGTAAAGCCAATCCCAGC 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86 lyLysThrIleSerAsnAspAspAspValGlnLysAlaAspValSerSer 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76 lArgGlnIleArg......GlnIleLysGluGlnG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 AspAsnPheAsnValLysProAspLysCysAlaIleLeuLysGluThrVa 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26 yGlnGlyLeuThrCysSerGlyGluLysArgArgArgGluGlnGluSerL 43 ::::||||::: ::: ::: :::
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383..2927
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                                                                                                                                                            Gaps:
                                                                                                                                                                892
                                                                                                                                                                                                                                                                                                                                841
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441	GlnMetSerGlyAlaArgTyrGlyGlySerSerAsnIleAlaSer ::: ::: ::: ::: ::: ::: ::: ::: ::: :::	427 1715
426 1714	InmetProSerSerArgAlaTyrGlyLeuAlaAspProSerThrThrGly :::	410 1665
1664	yCysAsnSerSerValGlyGlyMetSerMetSerProAsnGlnGlyLeuG : : : : : : :	393 1636
393 1635	ArgProAsnProAsnProValGlyGlnGlyIleArgProProMetAlaGl	377 1586
376	rgHisGlyPheValSerThrHisPheLeuGlnArgGluGlnAsnGlyTyr:::: :::	360 1551
1550	1ThrAlaGlnThrLysSerLysLeuPheArgAsnProValThrAsnAspA aACT CAGAGACCACTAACAGATGAGG	343 1525
1524		327 1505
326	lyGlnSerTrpSerGlnLysA ::: ::: GATGGACTTGGGTCCAGTCT.	310 1458
310 1457	ArgCysIleGlnArgPhePheSerLeuAsnAspG ::: :::::: ::: ACTGGAGAAAGTGGCATGATAGTTTTCCGGCTTCTTACAAAAAACAACC	299 1408
298 1407	CATGCAGCTGATATGCTTTATTGTGCCGAGTCCCATATCCGAATGATTAA	297 1358
1357	leAspThrAsnSerLeuArgSerSerMetArgProGlyPheGluAspIle :::: ::::	280 1308
280	AspLeuSerGlyLysValValAsnI ::: :::: ACTAGACTTCACACCTATTGGTTGTGATGCCAAAGGAAGAATTGTTTTAG	272 1258
271 \ 1257	SerPheIleThrargHis	266 1208
1 265	TTCCACCTCAGTTGGCTTTGTTTGCGATAGCTACTCCACTTCAGCCACCA	261 1158
11	GTTAAAGTATCTTCATGGACAGAAAAAGAAAGGG	1108
260		260
260	ArgIleThrThrGlyGluArgThrPhe	252 1058
251 1057	etGluGluGlyGluAspLeuGlnSerCysMetIleCysValAlaArg :::::	236 1008
1 236	nArgTyrGluThrMetGlnCysPheAlaLeuSerGlnProArgAlaMetM ::: :::	219 967

734	spGlyAsnValValLysGlnGluGlnLeuSerProLysLysGluAsn	718
2411	TTGTCCACAGCAAGACCCACAACAATATAATGTCTTTACAG	2371
718	lnAlaThrGlyLysAspThrSerSerIle	701
701 2370	LeuHisLysLeuLeuGlnAsnGlyAsnSerProAlaGluValAlaLysII ::::: ::::::: GTTAATGGCATGTTTGAAAATTGGAACTCTAACCAAATCGTGCCTTTCAA	685 2321
w	:::::: ::::: :::::::::::::::::::::::	2271
684	SerThrSerAsnMetHisGlySerLeuLeuGlnGlu.LysHi	668
668 2270	ServalThrSerProSerGlyValSerSerSerThrSerGlyGlyValSe:::	652 2221
2220 .	TTGGCTCTGAACTCAAGCT	2181
651	pSerSerC	642
641 2180	pArgGlyHisSerSerLeuThrAsnSerPro :::::	631 2144
2143	TCCTGACGTATGTCCAAGA	2120
631	lnLeuLeuThrCysSerSer	615
2119		2119
614	erLysGluSerSerValGluGlyAlaGluAsnGlnArgGlyProLeuGlu	598
2119		2099
598	gAspHisLeuSerAs	582
2098	:: :: GTGAGGTTGACTTC	7
582	spSerLysS	566
0 0	::::::: AAGACATCAGACACATGC	w
565	CIAGGCAIIGAITTT	549
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2016	CAGCA	1967
532	rSerSerSerLeuSerAlaLeuGlnAlaIleSer	518
1966	TGTGAACTCATTTGCTGGAGGTCACCCA	1919
517	isSerProMetAlaSerSerGlyAsnThrGlyAs	501
1918	::: 	1889
501	oArgAsnArgGlySerProLysIleAlaSerHisGlnPheSerProValA	484
1888	AATTGGCAAGATAATACTGCACCG	1865
484	erProGlyLeuAlaProAsnGlnGlnAsnIleMet	468
1864	::::::::::::::::::::::::::::::::::::::	1815
67	oSerSerTyrGlnAsnAsnAsnTyrGlyLeuAsnMetSerSerProPr	451
1814	TACTTCAAGT	1765
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| 2917 T 2917

	r 948	948
2916	CCACTTCATCATCCGTCAGAAGCCAGACCTTTTCCTGATTTGACATCCAG	2867
948	snSerAsnSerMetGlyArgProGlyGlyAspTyrAsnThrSe	932
2866	CCACACATCTTCAG	2853
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898		882
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2740.50 2554.81

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Database: Pending_Patents_NA_Main:*
Database sequences: 1316883
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Search information block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence Strd Orig ZScore EScore Len | Documentation cgn2_6/ptodata/1/pna/US090_COMB.seq:US-09-041-994-1 + 7383.00 6908.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -MODEL-frame+_p2n.model -DEV-x1p
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-041-994-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /pna/US095A_COMB.seq:US-09-513-066-1 +
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1.7e-133 6156
1.7e-133 6156
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US-09-041-994-2 x US-09-041-994-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
                                                                                                                                                       136 ACGCAAATTGCCATGTGATACTCCAGGACAAGGTCTTACCTGCAGTGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
186 AAAAACGGAGACGGGAGCAGGAAAGTAAATATATTGAAGAATTGGCTGAG
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                                                                                                                                                                                                                                                                                                                       86
                                                                 34 luLysArgArgGluGlnGluSerLysTyrIleGluGluLeuAlaGlu
                                                                                                                                                                                                                                                                                                                                                       1 MetSerGlyLeuGlyGluAsnLeuAspProLeuAlaSerAspSerArgLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
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                                                                                                                                                                                                                                                                                                                  ATGAGTGGATTAGGAGAAAACTTGGATCCACTGGCCAGTGATTCACGAAA 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality: 7383.00
Ratio: 5.218
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US-09-041-994-1 from: 1

to: 4496

50 185 34 Gaps: Percent Identity:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/09041994 GENERAL INFORMATION:
                                                                                                       TELEFAX: 617-742-4214
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                            ZIP: UZIVA
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-227-7400
TELEFAX: 617-742-4214
                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Liepmann, W. Hugo
REGISTRATION NUMBER: 20,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Chen, J. Don
APPLICANT: Li, Hui
TITLE OF INVENTION: Trai
TITLE OF INVENTION: Hori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
MOLECULE TYPE: cDNA
                                                                                        SEQUENCE CHARACTERISTICS:
                                TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Boston
                                                                     4496 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lahive and Cockfield
                                                                                                                                                                                                                                                             435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hormone Receptors
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                                                                                                                                                                                                                                                                                              US/09/041,994
                                                                                                                                                                                                    20,407
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3835 1267 3885	INC. INC.	3786 3786 1251 3836
3 7 10	SnAlaGlnMetValAlaGlnArgSerArgGluLeuLeuSerHisHis 	73
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Align seg 1/1

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US-09-513-066-1

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Ratio:
Percent Similarity:
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CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: USSN 09/041,994
PRIOR FILING DATE: 1998-03-13
PRIOR APPLICATION NUMBER: USSN 60/073,674
PRIOR FILING DATE: 1998-02-04
VOUNBER OF SEQ ID NOS: 37
SOFTMARE: PATENTIN VET: 2.0
SEQ ID NO 1
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US-09-041-994-2
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                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Chen, J. Don
APPLICANT: Leo, Christopher
APPLICANT: Li, Hui
TITLE OF INVENTION: NOVEL USE
TITLE OF INVENTION: STEROID N
FILE REFERENCE: UMG-026CP
                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (86)..(4330)
S-09-513-066-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4186
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x US-09-513-066-1
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                                              Percent
                                            Identity:
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        PLysCysAlaIleLeuLysGluThrValArgGlnIleArgGlnIleLysG

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        TAAATGTGCGATTTTAAAGGAAACAGTAAGACAGATACGTCAAATAAAAG

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600 1885	etCysGlnSerAsnSerArgAspHisLeuSerAspLysGluSerLysGlu	584 1836
584	rLysSerProLeuGlyPheTyrCysAspGlnAsnProValGluSerSerM	567
1835		1786
567	SerProAsnMetAsnIleThrGlnProSerLysValSerAsnGlnAspSe	551
1785		1736
550	lyThrSerLeuLeuSerThrLeuSerSerProGlyProLysLeuAspAsn	534
1735		1686
534	rPheSerSerSerLeuSerAlaLeuGlnAlaIleSerGluGlyValG	517
1685		1636
517 1635	AlaGlyValHisSerProMetAlaSerSerGlyAsnThrGlyAsnHisSe	501 1586
500	roArgAsnArgGlySerProLysIleAlaSerHisGlnPheSerProVal	484
1585		1536
484	OHISGlySerProGlyLeuAlaProAsnGlnGlnAsnIleMetIleSerP	467
1535		1486
467	ProSerSerTyrGlnAsnAsnAsnTyrGlyLeuAsnMetSerSerProPr	451
1485		1436
450	lyGlySerSerAsnIleAlaSerLeuThrProGlyProGlyMetGlnSer	434
1435		1386
434	rGlyLeuAlaAspProSerThrThrGlyGlnMetSerGlyAlaArgTyrG	417
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417	MetSerMetSerProAsnGlnGlyLeuGlnMetProSerSerArgAlaTy	401
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400 1285	lyGlnGlyIleArgProProMetAlaGlyCysAsnSerSerValGlyGly	384 1236
384 1235	sPheLeuGlnArgGluGlnAsnGlyTyrArgProAsnProAsnProValG	367 1186
367	LeuPheArgAsnProValThrAsnAspArgHisGlyPheValSerThrHi	351
1185		1136
350	rgPheSerLeuAlaAspGlyThrIleValThrAlaGlnThrLysSerLys	334
1135		1086
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1035		986
985	CACTGAGATCCTCCATGAGGCCTGGCTTTGAAGATATAATCCGAAGGTGT	936

884 2735 900 2785	rProProVallysAsnIleSeralaPheProMetLeuProLysGlnProM 	867 2686 884 2736
867 2685	ProTyrAsnArgAlaValSerLeuAspSerProValSerValGlySerSe	851 2636
850 ·	hråsnSerLeuGlyLeuLysSerSerGlnSerValGlnSerIleArgPro	834
2635		2586
834	eSerSerAsnGlySerHisLeuGlyThrLysGlnGlnValPheGlnGlyT	817
2585		2536
817	AspAlaIleLeuGlyAspLeuThrSerSerAspPheTyrAsnAsnSerIl	801
2535		. 2486
800	ysIleLysThrGluThrSerGluGluGlySerGlyAspLeuAspAsnLeu	784
2485		2436
784	rGlnCysThrSerSerThrIleProSerSerSerGlnGluLysAspProL	767
2435		2386
767	LeuSerLysGluLeuGlnProGlnValGluGlyValAspAsnLysMetSe	751
2385		2336
750	SNASNAlaLeuLeuArgTyrLeuLeuAspArgAspAspProSerAspAla	734
2335		2286
734	YASPG1YASnValValLYSG1nGluG1nLeuSerProLYSLYSLYSG1uA	717
2285		2236
717	IleThrAlaGlnAlaThrGlyLysAspThrSerSerIleThrSerCysGl	701
2235		2186
700	leLeuHisLysLeuLeuGlnAsnGlyAsnSerProAlaGluValAlaLys	. 684
2185		2136
684	lSerSerThrSerAsnMetHisGlySerLeuLeuGlnGluLysHisArgI	667
2135		2086
667	ValSerValThrSerProSerGlyValSerSerSerThrSerGlyGlyVa	651
2085		2036
650	isSerSerLeuThrAsnSerProLeuAspSerSerCysLysGluSerSer	634
2035		1986
634	YHISLYSLYSLeuLeuGlnLeuLeuThrCysSerSerAspAspArgGlyH	617
1985		1936
617 1935	SerSerValGluGlyAlaGluAsnGlnArgGlyProLeuGluSerLysGl	1886

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                                                                                                          oLysGlnLeuArgMetGlnLeuGlnGlnArgLeuGlnGlyGlnGlnPheL 1184
                                                                                                                                                     CAAGGAATGCACCCACGAGCCAACATCATGAGACCCCGGACAAACACCCC
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                                                                                                                                                                                                               AlaValMetMetAspGlnLysAlaGlyLeuTyrGlyGlnThrTyrProAl 1117
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GlyGlyAlaAlaValMetArgProMetMetGlnProGlnGlnGlyPheLe
                                              euAsnGlnSerArgGlnAlaLeuGluLeuLysMetGluAsnProThrAla
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                               TGAATCAGAGCCGACAGGCACTTGAATTGAAAATGGAAAACCCTACTGCT
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; LENGTH: 6835
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAMEXKEY: CDS
LOCATION: (201)..(4463)
US-09-125-635-1
                                                                                                                                                                                                                                                                seq_documentation_block:
    Sequence 1, Application US/09125635
    GENERAL INFORMATION:
    APPLICANT:    THE UNITED STATES OF AMERICA represented
    TITLE OF INVENTION:    AIB1, A novel steriod receptor c
    FILE REFERENCE: 49944
                                                                                                                                                                                                                                                                                                                                                                                                 seq_name:
                                                                                                           SOFTWARE: Pace
SEQ ID NO 1
FRIGHT: 6835
                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/125,635
CURRENT FILING DATE: 1998-08-21
PRIOR APPLICATION NUMBER: 60/049,728
PRIOR FILING DATE: 1997-06-17
NUMBER OF SEQ ID NOS: 12
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alignment_scores:
Quality: 7352.50
Ratio: 5.200
Percent Similarity: 99.577
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251 ArgArgIleThrThrGlyGluArgThrPheProSerAsnProGluSerPh
                                                                                                                                                                                                                                                                                                           AspLeuValAsnThrSerValTyrAsnIleLeuHisGluGluAspArgLy
                                                                                                            hrasnGluProGlnArgGlnLysSerHisThrPheasnCysArgMetLeu
|||||||||
|CAAATGAGACCCAAAGACAAAAAAGCCATACATTTAATTGCCGTATGTTG
                         laMetMetGluGluGlyGluAspLeuGlnSerCysMetIleCysValAla
                                              SerSerThrGlyGlnGlyValIleAspLysAspSerLeuGlyProLeuLe
                CTATGATGGAGGAAGGGGAAGATTTGCAATCTTGTATGATCTGTGGCA
                                                                                                                                                                             GACCTGGTTAACACAAGTGTTTACAATATCTTACATGAAGAAGACAGAAA
                                                                                                                                                                                                                                                                            TCTTCTACAGGGCAGGGAGTTATTGATAAAGACTCCTTAGGACCGCTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length: 1420
Gaps: 1
Percent Identity: 99.366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to:
                              250
                                                              234
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               950
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551 Ser 	534 lyT 1801 GGA	517 rPh 1751 CTT	501 Ala 1701 GCA	484 roa + 1651 CTC	467 OHI 1601 ACA	451 Pro 1551 CCA	434 lyg 1501 GGG	417 rG1 1451 rGG	401 Met 1401 ATG	384 lyG 	367 sph 1301 CTT	351 Leu 1251 CTC	334 rgP 1201 GAT	317 gHi 1151 TCA	301 Ile 1101 ATT	284 erL 1051 CAC	267 eII 1001 TAT	951 CGC
ProAsnMetAsnIleThrG	hrSerLeuLeuSerThrLe 	eSerSerSerLeuSer 	.GlyValHisSerProMetA 	xgAsnArgGlySerProLy 	SGlySerProGlyLeuAla 	SerSerTyrGlnAsnAsnA 	SerSerAsnIleAlaSe 	yLeuAlaAspProSerThr CTTGGCAGACCCTAGCACC	SerMetSerProAsnGlnG 	lnGlyIleArgProProMe 	eLeuGlnArgGluGlnAsn CCTTCAGAGAGAACAGAAT	PheArgAsnProValThrA TTCCGAAATCCTGTAACAA	heSerLeuAlaAspGlyThr - - - - - - - - - - - - - - - - - - -	.STYrGlnGluAlaTyrLeuAs 	GlnargPhePheSerLeua 	euArgSerSerMetArgPr 	eThrArgHisAspLeuSerG 	
lnProSerLysValSerAsr	uSerSerProGlyProLysL 	AlaLeuGlnAlaIleSerGl 	laSerSerGlyAsnThrGly 	SIleAlaSerHisGlnPheS GATAGCCTCACATCAGTTTT	ProAsnGlnGlnAsnIleMe 	.snTyrGlyLeuAsnMetSer 	rLeuThrProGlyProGlyM 	ThrGlyGlnMetSerGlyAl 	lyLeuGlnMetProSerSer 	tAlaGlyCysAsnSerSerV 	GlyTyrArgProAsnProAs 	.snAspArgHisGlyPheVal 	rIleValThrAlaGlnThrL TATAGTGACTGCACAGACAA	AsnGlyHisAlaGluThrPr 	\ASnAspGlyGlnSerTrpSer AATGATGGGCAGTCATGGTCC	:OGlyPheGluAspIleIleA !TGGCTTTGAAGATATAATCC	GlyLysValValAsnIleAs GAAAGGTTGTCAATATAGA	
nGlnAspSe	LeuAspAsn TGGATAAC	luGlyValG AAGGTGTGG	yAsnHisSe SAACCACAG	SerProVal	etIleSerP GATTTCTC	rSerProPr AGCCCCCC	MetGlnSer ATGCAATCA	laArgTyrG CTAGGTATG	PATGALATY CAGGGCCTA	ValGlyGly STAGGCGGC	SnProValG ATCCTGTTG	LSerThrHi TCAACCCA	LysSerLys AAAAGCAAA	COVALTYTA AGTATATC	rGlnLysAr CAGAAACG	ArgArgCys CGAAGGTGT	BPThrAsnS \TACAAATT	
567	550 1850	534 1800	517 1750	500 1700	484 1650	467 1600	450 1550	434 1500	417 1450	400 1400	384 1350	367 1300	350 1250	334 1200	317 1150	300	28 4 1050	1000

67	851 ProTyrAsnArgAlaValSerLeuAspSerProValSerValGlySerS
850 2750	834 hrasnSerLeuGlyLeuLysSerSerGlnSerValGlnSerIleargPro
834	817 eSerSerAsnGlySerHisLeuGlyThrLysGlnGlnValPheGlnGlyT
2700	
817	801 AspalaileLeuglyAspLeuThrSerSerAspPheTyrAsnAsnSerIl
2650	
800	784 ysilelysThrGluThrSerGluGluGlySerGlyAspLeuAspAsnLeu
2600	
784	767 rGlnCysThrSerSerThrIleProSerSerSerGlnGluLysAspProL
2550	
767	751 LeuSerLysGluLeuGlnProGlnValGluGlyValAspAsnLysMetSe
2500	
750	734 snäsnälaLeuLeuargTyrLeuLeuaspärgaspäspproSeräspäla
2450	
734	717 yaspGlyasnValValLysGlnGluGlnLeuSerProLysLysLysGluA
2400	
717	701 IleThralaGlnAlaThrGlyLysAspThrSerSerIleThrSerCysGl
2350	:::
700 2300	684 leLeuHisLysLeuLeuGlnAsnGlyAsnSerProAlaGluValAlaLys
684	667 lSerSerThrSerAsnMetHisGlySerLeuLeuGlnGluLysHisArgI
2250	
667	651 ValSerValThrSerProSerGlyValSerSerSerThrSerGlyGlyVa
2200	
650	634 ISSerSerLeuThrasnSerProLeuAspSerSerCysLysGluSerSer
2150	
63 4	617 yHislysLysLeuLeuGlnLeuLeuThrCysSerSerAspAspArgGlyH
2100	
617	601 SerSerValGluGlyAlaGluAsnGlnArgGlyProLeuGluSerLysGl
2050	
600	584 etcysg1nSerasnSerargAspH1sLeuSerAspLysg1uSerLysg1u
2000	
584	567 rlysSerProLeuGlyPheTyrCysAspGlnAsnProValGluSerSerM
1950	
1900	1851 TCTCCCAATATGAATATTACCCAACCAAGTAAAGTAAGCAATCAGGATTC

115	13	111	110	108	106	105	103	101	100	315	96	95	93	91	90	285	86
365		355	350	345	340	335	330	325	320	98	310	305	300	295	290	285	280
51 GlnGlyMetHisProArgAlaAsnIleMetArgProArgThrAsnThrP	34 erPheAsnSerMetMetAsnGlnMetAsnGlnGlnGlyAsnPheProLe	17 aGlnGlyProProMetGlnGlyGlyPheHisLeuGlnGlyGlnSerPro	01 AlaValMetMetAspGlnLysAlaGlyLeuTyrGlyGlnThrTyrProA	84 lnGlyGlnAlaLeuGluProLysGlnAspAlaPheGlnGlyGlnGluAl	67 rGlyLeuGluGluIleAspArgAlaLeuGlyIleProGluLeuValAsn	51 ArgalaLeuLeuAspGlnLeuHisThrLeuLeuSerAsnThrAspAlaT	34 euAspAspLeuValGlyProProSerAsnLeuGluGlyGlnSerAspG1	17 tGluGlnValSerHisGlyThrGlnAsnArgProLeuLeuArgAsnSer	01 AlaAlaAlaSerAsnGlnLeuGlySerTrpProAspGlyMetLeuSerM	84 etArgProGlyGluIleProMetGlyMetGlyAlaAsnProTyrGlyGl	7 rIleProGlyAlaArgProValLeuGlnGlnGlnGlnGlnMetLeuGl	51 ArgProAlaLeuGlyGlySerIleProThrLeuProLeuArgSerAsnS	34 snSerAsnSerMetGlyArgProGlyGlyAspTyrAsnThrSerLeuPr	17 rGlyAspTrpGlyLeuProAsnSerLysAlaGlyArgMetGluProMet	01 SerMetGlyGlyProAsnArgAsnValThrValThrGlnThrProSerS	84 etLeuGlyGlyAsnProArgMetMetAspSerGlnGluAsnTyrGlySe	67 rProProValLysAsnIleSerAlaPheProMetLeuProLysGlnPro
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r 1167 C 3700	u 1150 3650	S 1134 T 3600	1 1117 3550	a 1100 a 3500	G 1084 3450	h 1067 C 3400	u 1050 A 3350	L 1034	le 1017	n 1000 3200	.nM 984 .AA 3150	ie 967 G 3100	o 950 3050	A 934 I A 3000	e 917 C 2950	r 900 2900	M 884 2850

1184

euAsnGlnSerArgGlnAlaLeuGluLeuLysMetGluAsnProThrAla 1200

TGAATCAGAGCCGACAGGCACTTGAATTGAAAATGGAAAACCCTACTGCT 3800

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seq_documentation_block:
    Sequence 1, Application US/60068511
    GENERAL INFORMATION:
    APPLICANT: Suen, Chen-Shian
    APPLICANT: Frail, Donald E.
    APPLICANT: Lyttle, Richard C.
    APPLICANT: Cloning and
                                                                                                                                          seq_name: /cgn2_6/ptodata/1/pna/US6006_COMB.seq:US-60-068-511-1
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                                                                                                                                                                                                                                                                                                                AATGASnSerSerPheSerGlnGlnGlnPheAlaHiSGlnGlyAsnProA 1379
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                                                                                                                                                                                                                                                                   MetAsnMetAsnProMetProMetSerGlyMetProMetGlyProAspGl 1412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SerIleTyrGlnSerSerGluMetLysGlyTrpProSerGlyAsnLeuAl 1362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 erArgMetGlyProSerGlnAsnProMetMetGlnHisProGlnAlaAla 1345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OASPPTOAlaPheGlyArgValSerSerProProAsnAlaMetMetSerS 1329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GlyGlyAlaAlaValMetArgProMetMetGlnProGlnGlnGlyPheLe 1217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAAGAATGGGTCCCTCCCAGAATCCCATGATGCAACACCCCGCAGGCTGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGATCCAGCCTTTGGTCGAGTGTCTAGTCCTCCCAATGCAATGATGTCGT 4200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCTCCGCAACAGTTTCCATATCAACCAAATTATGGAATGGGACAACAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ProProGlnGlnPheProTyrGlnProAsnTyrGlyMetGlyGlnGlnPr 1312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTTCCCCCAGCATGGATGGGCTTTTGGCAGGACCCACAATGCCACAAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            laSerProSerMetAspGlyLeuLeuAlaGlyProThrMetProGlnAla 1295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       uAsnAlaGlnMetValAlaGlnArgSerArgGluLeuLeuSerHisHisP 1234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGTGGTGCTGCGGTGATGAGGCCTATGATGCAGCCCCCAGCAGGGTTTTCT
                                                                                                                                                                             GAAATACTGC 4460
                                                                                                                                                                                                                                                  ATGAACATGAACCCCATGCCCATGTCTGGCATGCCTATGGGTCCTGATCA 4450
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCCATCTATCAGTCCTCAGAAATGAAGGGCTGGCCATCAGGAAATTTGGC
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Cloning and Expression
 of a Nuclear
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alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; LOCATION:
US-60-068-511-1
                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: US-60-068-511-1
                                                                                                                                                                                                                                                                                                                                                                    US-09-041-994-2 x US-60-068-511-1
                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPAX: 973-683-4117
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4789 base pairs
                                                                                                                                                                                                                                                                         HYPOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: 973-683-2169
                                                                                          335
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NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Walsh, Andrea C.
REGISTRATION NUMBER: 34,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                               385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                       51
                                                                                                                                                                                                              MOLECULE TYPE: CDNA
                                                          67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 07054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Parsippany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                       LeuIleSerAlaAsnLeuSerAspIleAspAsnPheAsnValLysProAs 67
luGlnGlyLysThrIleSerAsnAspAspAspValGlnLysAlaAspVal 100
                                                                                          CTGATATCTGCCAATCTTAGTGATATTGACAATTTCAATGTCAAACCAGA
                               TAAATGTGCGATTTTAAAGGAAACAGTAAGACAGATACGTCAAATAAAAG
                                               pLysCysAlaIleLeuLysGluThrValArgGlnIleArgGlnIleLysG
                                                                                                                                                                                                                                                                                                                                                                                                                Quality: 7341.00
Ratio: 5.192
milarity: 99.368
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185..4750
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384	367 1285	351 1235	334 1185	317 1135	301 1085	284 1035	267 985	251 935	234 885	217 835	201 785	184 735	167 685	151 635	134 585	117 535	101 485	435
6	67 sPheLeuGlnArgGluGlnAsnGlyTyrArgPr 	ົພ ທ	α ω	ω Ë	æ ö	ω α	œ 6	ω in	eo iu	$\tilde{\omega}$	01 MetLysThrProHisAspIleLeuGluAspIleAsnAla 	ω co	67 saspPheLeuLysasnLeuProLysSerThrValasnGl 	ات نت	34 leValPheValSerGluAsnValThrGlnTyrLeuGlnT 	17 uLeuGlnAlaLeuAspGlyPheLeuPheValValAsnAr 35 ACTTCAGGCATTGGATGGTTTCCTATTTGTGGTGAATCG	8 0	(LL)
erValGlyGly 	OASnProValG AAATCCTGTTG	ValSerThrHi gTCTCAACCCA	hrLysSerLys CAAAAGCAAA	rProValTyrA CCAGTATATC	SerGlnLysAr CCCAGAAACG	leArgArgCys TCCGAAGGTGT	eAspThrAsnS AGATACAAATT	ProGluSerPh CCTGAGAGCTT	leCysValAla TCTGTGTGGCA	rGlnProArgA TCAGCCACGAG	SerProGluMe AGTCCTGAAAT	ysargMetLeu CCCGTATGTTG	yValSerTrpT AGTTTCCTGGA	GluAspArgLy GAAGACAGAAA	YrLysGlnGlu ATAAGCAAGAG	gGluAlaAsnī :::::: AGACGGAAACA	GlyProLeuLe GACCGCTTTT	
400	384 1334	367 1284	350 1234	334 1184	317 1134	300 1084	284 1034	267 984	250 934	23 4 884	217 834	200 784	184 734	167 684	150 634	134 584	117 534	484
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	1000	etArgProGlyGluIleProMetGlyMetGlyAlaAsnProTyrGlyGln	984
	3184		3135
	984	rIleProGlyAlaArgProValLeuGlnGlnGlnGlnGlnMetLeuGlnM	967
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	950 3034	snSerAsnSerMetGlyArgProGlyGlyAspTyrAsnThrSerLeuPro	934 2985
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	2984		2935
	917 2934	SerMetGlyGlyProAsnArgAsnValThrValThrGlnThrProSerSe	901 2885
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1292 4084	SNValThrAlaSerProSerMetAspGlyLeuLeuAlaGlyProThrMet	1276 4035
1276	nGlnGlnGlnGlnGlnGlnGlnThrGlnAlaPheSerProProProA	1259
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3234		3185

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Sequence 3962, Application Us/09359922

GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: MOVEL CONTIGS OBTAINED FRO
TITLE OF INVENTION: LIBRARIES
FILE REFERENCE: 20411-752CON1
CURRENT APPLICATION NUMBER: US/09/359,922
CURRENT FILING DATE: 1999-07-22
CURRENT FILING DATE: 1998-12-03
EARLIER APPLICATION NUMBER: US 09/205,155
EARLIER FILING DATE: 1998-12-03
NUMBER OF SEQ ID NOS: 13203
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3962
                                                                                                                                                                      alignment_block:
US-09-041-994-2 x US-09-359-922-3962
                                                                                                                                                                                                                                                                    ; FEATURE:
, NAME/KEY: misc_feature
; LOCATION: (1)...(6855)
; OTHER INFORMATION: n =
US-09-359-922-3962
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                                                                                                                                                                                                CTATGATGGAGGAAGGGGAAGATTTGCAATCTTGTATGATCTGTGGCA
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0	567	SerProAsnMetAsnIleThrGlnProSerLysValSerAsnGlnAspSe	551
	1900		1851
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	1850		1801
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	1800		1751
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684	lSerSerThrSerAsnMetHisGlySerLeuLeuGlnGluLysHisArgI	667
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667	ValSerValThrSerProSerGlyValSerSerSerThrSerGlyGlyVa	651
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650	isSerSerLeuThrAsnSerProLeuAspSerSerCysLysGluSerSer	634
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                                                                                                                                          lnGlyGlnAlaLeuGluProLySGlnAspAlaPheGlnGlyGlnGluAla
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                                                                                                                                                                                                                                                                                                                                                                         euAspAspLeuValGlyProProSerAsnLeuGluGlyGlnSerAspGlu
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TYPE: DNA
CORCANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(6855)
OTHER INFORMATION: n = A
US-09-359-922-3962

Α,Τ, 'n or G

LENGTH: 6855

FROM

VARIOUS

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Sequence 3962, Application US/09359922A
GENERAL INFORMATION:
APPLICANT: Leshkowitz, Dena
APPLICANT: Liu, Jin
APPLICANT: Liu, Jin
ITILE OF INVENTION: NOVEL CONTIGS OBTAINED FRO
TITLE OF INVENTION: LIBRARIES
FILE REFERENCE: 20411-752CON1
CURRENT APPLICATION NUMBER: US/09/359,922A
CURRENT FILING DATE: 1999-07-22
EARLIER APPLICATION NUMBER: US 09/205,155
EARLIER FILING DATE: 1998-12-03
EARLIER FILING DATE: 1998-12-03
EARLIER FILING DATE: 1998-02-13
NUMBER OF SEQ ID NOS: 13203
SOFTWARE: FastSEQ for Windows Version 3.0
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Percent Identity: 99.087
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534 lyThrSerLeuLeuSerThrLeuSerSerProGlyPr	.701 GCAGGTGTGCACTCTCCCATGGCATCTTCTGGCAATA 517 rPheSerSerSerSerLeuSerAlaLeuGlnAlaIle	484 roArgAsnArgGlySerProLysIleAlaSerHisGl	467 OHISGLYSerProGlyLeuAlaProAsnGlnGlnAsn 	434 lyGlySerSerAsnIleAlaSerLeuThrProGlyPr	417 rGlyLeuAlaAspProSerThrThrGlyGlnMetSer 	401 MetSerMetSerProAsnGlnGlyLeuGlnMetProS 	384 lyGlnGlyIleArgProProMetAlaGlyCysAsnSe	367 sPheLeuGlnArgGluGlnAsnGlyTyrArgProAsn	351 LeuPheArgAsnProValThrAsnAspArgHisGlyP 	334 rgPheSerLeuAlaAspGlyThrIleValThrAlaGl 	317 9HisTyrGlnGluAlaTyrLeuAsnGlyHisAlaGlu 	301 IleGlnArgPhePheSerLeuAsnAspGlyGlnSerT 	284 erLeuArgSerSerMetArgProGlyPheGluAspIl 	267 eIleThrArgHisAspLeuSerGlyLysValValAsn 	
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.nAsnProValGluSerSerM 584	ProTyrAsnArgAlaValSerLeuAspSerPro	851 P 2751 C
ASIPTOVALGLUSETSETM ANTECAGTIGGAGAGTTCAA 19 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	hrasnSerLeuGlyLeuLysSerSerGlnSer	834 h 2701 C
ASDPTOVALGLUSETSETM	eSerSerAsnGlySerHisLeuGlyThrLysG 	817 e 1 2651 å
ASDPTOVALGLUSETSETM ANTICAGTIGGAGAGTTCAA 19 AATCCAGTIGGAGAGTTCAA 19 AATCCAGTIGGAGAGTTCAA 19 TASPLYSGLUSETLYSGL 60 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	ASPAlaIleLeuGlyASPLeuThrSerSerAsj 	801 P 2601 G
ASDPTOVALGLUSETSETM ANTICAGTIGGAGAGTTCAA 19 ANTICAGTIGGAGAGTTCAA 19 ANTICAGTIGGAGAGTTCAA 19 ANTICAGTIGGAGAGTTCAA 19 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	ysIleLysThrGluThrSerGluGluGlySer	784 y 1 2551 p
ASDPTOVALGLUSETSETM 58 ANTCCAGTGGAGAGTTCAA 19 ANTCCAGTGGAGAGTTCAA 19 ANTCCAGTGGAGAGTTCAA 19 ANTCCAGTGGAGAGTTCAA 19 ANTCCAGTGGAGAGTTCAA 19 ANTCCAGTGGAGAGTTCAA 19 ANTCCAGTGGAGAGTTCAGAGGAG 20 LYPTOLEUGLUSETLYSG1 61 LIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	rGlnCysThrSerSerThrIleProSerSerSiliiiiiiiiiiiiiiiiiiiiiiiiiiiiiii	767 r 2501 1
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Polym

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   GENERAL INFORMATION:
   APPLICANT: MOTIS, MacDonald
   APPLICANT: Lal, Preeti
   APPLICANT: Lal, Preeti
   APPLICANT: Diep, Dinh
   TITLE OF INVENTION: Method for the Ide
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US-09-041-994-2 x US-60-172-373-13551
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: US-60-172-373-13551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/60/172,373
CURRENT FILING DATE: 1999-12-16
NUMBER OF SEQ ID NOS: 25,772
SOFTWARE: PERL PROGram
SEQ ID NO 13551
LENGTH: 7956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide FILE REFERENCE: \mbox{GX-}0006 P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
 766
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       216 ATGAGTGGATTAGGAGAAAACTTGGATCCACTGGCCAGTGATTCACGAAA
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AspLeuValAsnThrSerValTyrAsnIleLeuHisGluGluAspArgLy
                                                                                                                                                                                                                                                                                               liGlnGlyLysThrIleSerAsnAspAspAspValGlnLysAlaAspVal

      pLysCysAlaIleLeuLysGluThrValArgGlnIleArgGlnIleLysG

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      TAAATGTGCGATTTTAAAGGAAACAGTAAGACAGATACGTCAAATAAAAG

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MetSerGlyLeuGlyGluAsnLeuAspProLeuAlaSerAspSerArgLy
                                                                      SASPPheLeuLySAsnLeuProLySSerThrValAsnGlyValSerTrpT
                                                                                                                                                                                                                                      ACTTCAGGCATTGGATGGTTTCCTATTTGTGGTGAATCGAGACGGAAACA
                                                                                                                                                                                                                                                     uLeuGlnAlaLeuAspGlyPheLeuPheValValAsnArgGluAlaAsnI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACGCAAATTGCCATGTGATACTCCAGGACAAGGTCTTACCTGCAGTGGTG
                                                          GGATTTTCTTAAGAATTTACCAAAATCTACAGTTAATGGAGTTTCCTGGA
                                                                                                                   GACCTGGTTAACACAAGTGTTTACAATATCTTACATGAAGAAGACAGAAA
                                                                                                                                                                             TTGTATTTGTATCAGAAAATGTCACACAATACCTGCAATATAAGCAAGAG
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5.184
99.228
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Gaps:
Percent Identity:
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500 1715	4 roArgAsnArgGlySerProLysIleAlaSerHisGlnPheSerProVal	48, 166
484 1665	7 OH18G1ySerProG1yLeuAlaProAsnGlnGlnAsnIleMetIleSerP	467 161
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1565		151
434 1515	7 rGlyLeuAlaAspProSerThrThrGlyGlnMetSerGlyAlaArgTyrG	41; 146
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384 1365	77 sPheLeuGlnArgGluGlnAsnGlyTyrArgProAsnProAsnProValG	36'
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1315		126
350	34 rgPheSerLeuAlaAspGlyThrIleValThrAlaGlnThrLysSerLys	33,
1265		121
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1215		116
317	11 IleGlnArgPhePheSerLeuAsnAspGlyGlnSerTrpSerGlnLysAr	30:
1165		111
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1115		106
284	57 eileThrArgHisAspLeuSerGlyLysValValAsnīleAspThrAsnS	26.
1065		101
267	11 ArgArgIleThrThrGlyGluargThrPheProSerAsn	25:
1015		96
250 965	4 laMetMetGluGluGlyGluAspLeuGlnSerCysMetIleCysValAla	23, 91
234 915	7 targGlnargTyrGluThrMetGlnCysPheAlaLeuSerGlnProArgA	217
217 865	1 MetLysThrProHisAspIleLeuGluAspIleAsnAlaSerProGluMe 	20:

801 AspAlaIleLeuG	784 ysileLysThrGl + +	767 rGlnCysThrSer 2516 TCAGTGCACCAGC	751 LeuSerLysGluL 	734 snAsnAlaLeuLeuA 2416 ATAATGCACTTCTTA	717 yAspGlyAsnVal 	701 IleThralaGlnA ::: 2316 ATTACTGCAGAAG	684 leLeuHisLysLe 1	667 lSerSerThrSer 2216 ATCCTCTACATCC	651 ValSerValThrS 	634 isSerSerLeuTh 2116 ATTCCTCCTTGAC	617 yHisLysLysLeu 1066 TCATAAAAAATTA	601 SerSerValGlug 2016 AGCAGTGTTGAGG	584 etCysGlnSerAs 1966 TGTGTCAGTCAAA	567 rLysSerProLeu 1916 CAAGAGTCCTCTG	551 SerProAsnMetAs 1866 TCTCCCAATATGAA	534 lyThrSerLeuLe 1816 GGACTTCCCTTTT	517 rPheSerSerSer 	501 AlaGlyValHisS 1716 GCAGGTGTGCACT
${f lyAspLeuThrSerSerAspPheTyrAsnAsnSerI}$.uThrSerGluGluGlySerGlyAspLeuAspAsnLe 	SerThrIleProSerSerSerGlnGluLysAspPro 	euGlnProGlnValGluGlyValAspAsnLysMet 	uArgTyrLeuLeuAspArgAspAspProSerAspAl TAGATACCTGCTGGACAGGGATGATCCTAGTGATGC	.VallysGlnGluGlnLeuSerProLysLysGlu 	laThrGlyLysAspThrSerSerIleThrSerCysG CACTGGGAAAGACACCAGCAGTATAACTTCTTGTG	uLeuGlnAsnGlyAsnSerProAlaGluValAlaLy GCTGCAGAATGGGAATTCACCAGCTGAGGTAGCCAA	AsnMetHisGlySerLeuLeuGlnGluLysHisArg 	erProSerGlyValSerSerSerThrSerGlyGlyV 	rAsnSerProLeuAspSerSerCysLysGluSerSe 	LeuGlnLeuLeuThrCysSerSerAspAspArgGly + + + + + +	lyAlaGluAsnGlnArgGlyProLeuGluSerLysG 	mSerArgAspHisLeuSerAspLysGluSerLysGl 	GlyPheTyrCysAspGlnAsnProValGluSerSer 	SnIleThrGlnProSerLysValSerAsnGlnAspS 	uSerThrLeuSerSerProGlyProLysLeuAspAsn 	SerLeuSerAlaLeuGlnAlaIleSerGluGlyVal 	erProMetAlaSerSerGlyAsnThrGlyAsnHisS
1 817	u 800 A 2615	T 784 1 A 2565	Se 767 AG 2515	a 750 A 2465	A 734 A 2415	1 717 2365	's 700 G 2315	I 684 A 2265	a 667 2215	r 650 T 2165	H 634 C 2115	1 617 2065	u 600 G 2015	M 584 A 1965	e 567 C 1915	n 550 C 1865	G 534 G 1815	e 517 G 1765

8 GlnGluAlaAlaValMetMetAspGlnLysAlaGlyLeuTyrGlyGlnTh 1	31 euValAsnGlnGlyGlnAlaLeuGluProLysGlnAspAlaPheGlnGly 1097 	54 rAspAlaThrGlyLeuGluGluIleAspArgAlaLeuGlyIleProGluL 1081 	18 SerAspGluArgAlaLeuLeuAspGlnLeuHisThrLeuLeuSerAsnTh 1064 		4 tLeuSerMetGluGlnValSerHisGlyThrGlnAsnArgProLeuLeuA 1031 									37 rProProValLysAsnIleSerAlaPheProMetLeuProLysGlnProM 884 	31 ProTyrAsnArgAlaValSerLeuAspSerProValSerValGlySerSe 867 	34 hrAsnSerLeuGlyLeuLysSerSerGlnSerValGlnSerIleArgPro 850 	17 eSerSerAsnGlySerHisLeuGlyThrLysGlnGlnValPheGlnGlyT 834 	
1392 HismetGlyGlnmetAsnMetAsnPrometPrometSerGlymetProme 1408	1375 lnGlyAsnProAlaValTyrSerMetValHisMetAsnGlySerSerGly 1391	1358 rGlyAsnLeuAlaArgAsnSerSerPheSerGlnGlnGlnPheAlaHisG 1375	1342 ProGlnAlaAlaSerIleTyrGlnSerSerGluMetLysGlyTrpProSe 1358	1325 lametMetSerSerArgMetGlyProSerGlnAsnProMetMetGlnHis 1341	1308 tGlyGlnGlnProAspProAlaPheGlyArgValSerSerProProAsnA 1325	MetProGlnAlaProProGlnGlnPheProTyrGlnProAsnTyrGlyMe 	1275 roAsnValThrAlaSerProSerMetAspGlyLeuLeuAlaGlyProThr 1291	1258 nGlnGlnGlnGlnGlnGlnGlnGlnGlnThrGlnAlaPheSerProProP 1275	1244GlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnG	1227 rgGluLeuLeuSerHisHisPheArgGlnGlnArgValAlaMetMetMet 1243	1213GlnGlnGlyPheLeuAsnAlaGlnMetValAlaGlnArgSerA 1227	1198 ProThrAlaGlyGlyAlaAlaValMetArgProMetMetGlnPro 1212	1181 lnGlnPheLeuAsnGlnSerArgGlnAlaLeuGluLeuLysMetGluAsn 1197	1164 rAsnThrProLysGlnLeuArgMetGlnLeuGlnGlnArgLeuGlnGlyG 1181	1148 PheProLeuGlnGlyMetHisProArgAlaAsnIleMetArgProArgTh 1164	InSerProSerPheasnSerMetMetAsnGlnMetAsnGlnGlnGlnGlyAsn		CAAGAAGCAGCAGTAATGATGGATCAGAAGGCAGGATTATATGGACAGAC

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Sequence 1, Application US/09440612
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Lex M. Cowsert
TITLE OF INVENTION: ANTISENSE MODULATION OF SRCFILE REFERENCE: RTS-0042
CURRENT APPLICATION NUMBER: US/09/440,612
CURRENT FILING DATE: 1999-11-15
NUMBER OF SEQ ID NOS: 47
SEQ ID NO 1
LENGTH: 6754
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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Quality: 7
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; NAME/KEY: CDS
; LOCATION: (184)..(4422)
US-09-440-612-1
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US-09-041-994-2 x US-09-440-612-1
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                                                                                                                                                                                                                                                                                                                              284 AAAAACGGAGACGGGAGCAGGAAAGTAAATATTGAAGAATTGGCTGAG
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                                                                                                          luGlnGlyLysThrIleSerAsnAspAspAspValGlnLysAlaAspVal 100
                                                                                                                                                                                                                                                                        CTGATATCTGCCAATCTTAGTGATATTGACAATTTCAATGTCAAACCAGA
                                                                                                                                                              AGCAAGGAAAAACTATTTCCAATGATGATGTTCAAAAAGCCGATGTA 483
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5.175
97.968
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Percent Identity: 97.758
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457	erLeuThrProGlvProGlvMetGlnSerProSerSerTvrGlnAsnA	4
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424 148	nGlyLeuGlnMetProSerSerArgAlaTyrGlyLeuAlaAspProSerT 	407 1434
407 143	MetAlaGlyCysAsnSerSerValGlyGlyMetSerMetSerProAsnGl 	391 1384
390 138	snGlyTyfArgProAsnProAsnProValGlyGlnGlyIleArgProPro	374 1334
374 133	rAsnAspArgHisGlyPheValSerThrHisPheLeuGlnArgGluGlnA 	357 1284
357 128	ThrileValThrAlaGlnThrLysSerLysLeuPheArgAsnProValTh	341 1234
	roValTyrArgPheSe CAGTATATCGATTCTC	324 1184
324 118	CCAGTGATGGGATATTTTCCCCAA	317 1134
317 113	euAs TAAA	301 1084
300 108	erLeuArgSerSerMetArgProGlyPheGluAspIleIleArgArgCys 	284 1034
284 103	eIleThrargHisAspLeuSerGlyLysValValAsnIleAspThrAsnS 	267 984
267 983	ArgArgIleThrThrGlyGluArgThrPheProSerAsnProGluSerPh 	251 934
250 933	laMetMetGluGluGlyGluAspLeuGlnSerCysMetIleCysValAla 	23 4 88 4
234 883	tArgGlnArgTyrGluThrMetGlnCysPheAlaLeuSerGlnProArgA	217 834
217 833	MetLysThrProHisAspIleLeuGluAspIleAsnAlaSerProGluMe 	201 784
200 783	hrAsnGluProGlnArgGlnLysSerHisThrPheAsnCysArgMetLeu 	184 734
184 733	SASPPheLeuLysAsnLeuProLysSerThrValAsnGlyValSerTrpT 	167 684
167 683	ASPLeuValAsnThrSerValTyrAsnTleLeuHisGluGluAspArgLy	151 634

741	724 2384	707 2334	.691 2284	674 2234	657 2184	641 2134	624 2084	607 2034	591 1984	574 1934	557 1884	541 1834	524 1784	507 1734	491 1684	474 1634	457 1584	1534
LeuLeuAspArgAspAspProSerAspAlaLeuSerLysGluLeuGlnPr 757 	lnGluGlnLeuSerProLysLysGluAsnAsnAlaLeuLeuArgTyr 740 	yLysAspThrSerSerIleThrSerCysGlyAspGlyAspValValLysG 724 	AsnGlyAsnSerProAlaGluValAlaLysIleThrAlaGlnAlaThrGl 707 	isGlySerLeuLeuGlnGluLysHisArgIleLeuHisLysLeuLeuGln 690 	rGlyValSerSerSerThrSerGlyGlyValSerSerThrSerAsnMetH 674 	ProLeuAspSerSerCysLysGluSerSerValSerValThrSerProSe 657 	euLeuThrCysSerSerAspAspArgGlyHisSerSerLeuThrAsnSer 640 	uAsnGlnArgGlyProLeuGluSerLysGlyHisLysLysLeuLeuGlnL 624 	AspHisLeuSerAspLysGluSerLysGluSerSerValGluGlyAlaGl 607 	yrCysAspGlnAsnProValGluSerSerMetCysGlnSerAsnSerArg 590 	rGlnProSerLysValSerAsnGlnAspSerLysSerProLeuGlyPher 574 	LeuSerSerProGlyProLysLeuAspAsnSerProAsnMetAsnIleTh 557 	eralaLeuGlnAlaIleSerGluGlyValGlyThrSerLeuLeuSerThr 540 	talaSerSerGlyAsnThrGlyAsnHisSerPheSerSerSerSerLeuS 524 	LysIleAlaSerHisGlnPheSerProValAlaGlyValHisSerProMe 507 	laProAsnGlnGlnAsnIleMetIleSerProArgAsnArgGlySerPro 490 	nAsnTyrGlyLeuAsnMetSerSerProProHisGlySerProGlyLeuA 474 	
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GlyProThrMetProGlnAlaProProGlnGlnPheProTyrGlnProAs
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LENGTH: 6754
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (184)..(4422)
US-09-440-612-3
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Quality:
Ratio:
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; Sequence 3, Applicatio
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                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: US-09-440-612-3 from:
                                                                                                                                                                                                                                                                                                                                                                               US-09-041-994-2 x US-09-440-612-3
                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Lex M. Cowsert
TITLE OF INVENTION:
FILE REFERENCE:
RTS-0042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS:
SEQ ID NO 3
LENGTH: 6754
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                                                                                               pLysCysAlaIleLeuLysGluThrValArgGlnIleArgGlnIleLysG
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                                                                                 TAAATGTGCGATTTTAAAGGAAACAGTAAGACAGATACGTCAAATAAAAG
                                                                                                                                     CTGATATCTGCCAATCTTAGTGATATTGACAATTTCAATGTCAAACCAGA
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                            AGCAAGGAAAAACTATTTCCAATGATGATGTTCAAAAAGCCGATGTA
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340 L233	euAsnGlyHisAlaGluThrProValTyrArgPheSerLeuAlaAspGly 3 	324 1184
324 1183	9H1sTyrGlnGluAlaTyrL 3	317 1134
317 L133	IleGlnArgPhePheSerLeuAsnAspGlyGlnSerTrpSerGlnLysAr 3	301 1084
300 L083	erLeuArgSerSerMetArgProGlyPheGluAspIleIleArgArgCys 3 	284 1034
28 4 L033	elleThratgHisaspLeuSerGlyLysValValasnIleAspThrasnS 2 	267 984
267 983	ArgArgIleThrThrGlyGluArgThrPheProSerAsnProGluSerPh 2	251 934
250	lametMetGluGluGlyGluAspLeuGlnSerCysMetIleCysValAla 2 	234 884
234 383	tArgGlnArgTyrGluThrMetGlnCysPheAlaLeuSerGlnProArgA 2	217 834
217 333	MetLysThrProHisAspIleLeuGluAspIleAsnAlaSerProGluMe 2 	201 784
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L84 733	SASPPheLeuLysAsnLeuProLysSerThrValAsnGlyValSerTrpT 1	167 684
L6 7 583	ASPLeuValAsnThrSerValTyrAsnIleLeuHisGluGluAspArgLy 1	151 634
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13 4 .	uLeuGlnAlaLeuAspGlyPheLeuPheValValAsnArgGluAlaAsnI 1 	117 534
533		484

69 228	. 67 223	65 218	64 213	208	60 203	59 198	57 193	55 188	54 183	52 178	50 173	49 168	47 163	45 158	44 153	42 148	40 143	138
1 AsnGlyAsnSerProAlaGluValAlaLysil 	4 isGlySerLeuLeuGlnGluLysHisArgIle 	7 rGlyValSerSerSerThrSerGlyGlyValS	1 ProLeuAspSerSerCysLysGluSerSerVa	4 euLeuThrCysSerSerAspAspArgGlyHis 	7 uAsnGlnArgGlyProLeuGluSerLysGlyH 	1 ASPHISLeuSerASpLySGluSerLySGluSe	4 yrCysAspGlnAsnProValGluSerSerMet 	7 rGlnProSerLysValSerAsnGlnAspSerLy 	1 LeuSerSerProGlyProLysLeuAspAsnSe 	4 erAlaLeuGinAlaIleSerGluGlyValGly	7 tAlaSerSerGlyAsnThrGlyAsnHisSerF 	1 LysIleAlaSerHisGlnPheSerProValA	4 laProAsnGlnGlnAsnIleMetIleSerPro 	7 nAsnTyrGlyLeuAsnMetSerSerProPro	1 SerLeuThrProGlyProGlyMetGlnSerPr	4 hrThrGlyGlnMetSerGlyAlaArgTyrGly	7 nG1yLeuGlnMetProSerSerArgAlaTyrG 	4 ATGGCTGGATGCAACAGTTCGGTAGGCGGCATG
eThralaGlnalaThrGl 707 ::: TACTGCAGAAGCCACTGG 233	LeuHisLysLeuLeuGln 690	erSerThrSerAsnMetH 674	lSerValThrSerProSe 657	SerSerLeuThrAsnSer 640	iisLysLysLeuGenn 624 	rSerValGluGlyAlaGl 607 	CysGlnSerAsnSerArg 590	ysSerProLeuGlyPheT 574 	rProAsnMetAsnIleTh 557	ThrSerLeuLeuSerThr 540	heSerSerSerLeuS 524	LaGlyValHisSerProMe 507 	ArgAsnArgGlySerPro 490)H1SG1ySerProG1yLeuA 474 	oSerSerTyrGlnasnas 457 	GlySerSerAsnIleAla 440 	lyLeuAlaAspProSerT 424 	GAGTATGTCGCCAAACCA 143

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2433		2384
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2383		2334

1305 nTyrGlyMetGlyGlnGlnProAspProAlaPheGlyArgVa	1289 GlyProThrMetProGlnAlaProProGlnGlnPheProTyr	1272 erProProProAsnValThrAlaSerProSerMetAspGlyLe 	1255 nglnglnglnglnglnglnglnglnglnglnglnglngln	1241 MetMetMetGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnG	1224 lnArgSerArgGluLeuLeuSerHisHisPheArgGlnGlnA 	1207 gPrometMetGlnProGlnGlnGlyPheLeuAsnalaGlnMe 	1191 LeuGluLeuLysMetGluAsnProThrAlaGlyGlyAlaAla 	1174 euGlnGlnArgLeuGlnGlyGlnGlnPheLeuAsnGlnSerA 	1157 aAsnIleMetArgProArgThrAsnThrProLysGlnLeuAr 	1141 GlnMetAsnGlnGlnGlyAsnPheProLeuGlnGlyMetHis 	1124 lyGlyPheHisLeuGlnGlyGlnSerProSerPheAsnSerMe 	1107 sAlaGlyLeuTyrGlyGlnThrTyrProAlaGlnGlyProPr 	1091 LysGlnAspAlaPheGlnGlyGlnGluAlaAlaValMetMet	1074 rgAlaLeuGlyIleProGluLeuValAsnGlnGlyGlnAlaLe 	1057 uHisThrLeuLeuSerAsnThrAspAlaThrGlyLeuGluGl 	1041 ProSerAsnLeuGluGlyGlnSerAspGluArgAlaLeuLeuA 	1024 hrGlnAsnArgProLeuLeuArgAsnSerLeuAspAspLeuV 	3189 GGGTTCCTGGCCCGATGGCATGTTGTCCATGGAACAAGTTTC
lserserP 1322	GlnProAs 1305 CAACCAAA 4088	euLeuAla 1288 TTTTGGCA 4038	nAlaPheS 1272 GGCCTTCA 3988	GlnGlnGl 1255 CAGCAGCA 3938	rgValAla 1240 GGGTGGCT 3888	tValAlaG 1224	ValMetAr 1207 GTGATGAG 3788	rgGlnAla 1190 GACAGGCA 3738	9MetGlnL 1174 AATGCAGC 3688	ProArgAl 1157 CCACGAGC 3638	@tMetAsn 1140 TGATGAAT 3588	OMetGlnG 1124 AATGCAAG 3538	AspGlnLy 1107 GATCAGAA 3488	euGluPro 1090 TAGAGCCC 3438	LUILEASPA 1074 AATTGACA 3388	ASPGINLE 1057 GACCAGCT 3338	/alGlyPro 1040 TTGGGCCA 3288	TCATGGCA 3238

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alignment_scores:
Quality:
Ratio:
Percent Similarity:
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TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES ANI
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.1186-001
CURRENT APPLICATION NUMBER: US/09/652,123
CURRENT EILING DATE: 2000-08-30
PRIOR APPLICATION NUMBER: 60/151,135
PRIOR APPLICATION NUMBER: 60/151,135
PRIOR FILING DATE: 1999-08-30
NUMBER OF SEQ ID NOS: 9796
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                   alignment_block:
US-09-041-994-2 x US-09-652-123-8947
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   Sequence 8947, Application US/09652123
   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Homo sapiens US-09-652-123-8947
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LENGTH: 7888
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LeuIleSerAlaAsnLeuSerAspIleAspAsnPheAsnValLysProAs
                                                             luLysArgArgArgGluGlnGluSerLysTyrIleGluGluLeuAlaGlu
                                                                                                    yMetProMetGlyProAspGlnLysTyrCys 1415
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                                                                                                                                                                                                                                                                                                                 hrAsnGluProGlnArgGlnLysSerHisThrPheAsnCysArgMetLeu
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      pLysCysAlaIleLeuLysGluThrValArgGlnIleArgGlnIleLysG

      |||||||||||||||||||||

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ThrIleValThrAlaGlnThrLysSerLysLeuPheArgAsnProValTh
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                                                                                                                                                                               CACTGAGATCCTCCATGAGGCCTGGCTTTGAAGATATAATCCGAAGGTGT 108:
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9	941	924	907	891	874	857	841	824	807	791	774	757	741	724	707	691	674	657
	2987	2937	2918	2882	2832	2782	2732	2682	2632	2582	2532	2482	2432	2382	2332	2282	2232	2182
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74	957	940	924	907	890	87 4	857	840	824	807	790	774	757	740	724	707	690	674
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                                                                                                                                                                                                                                GlnMetAsnGlnGlnGlyAsnPheProLeuGlnGlyMetHisProArgAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hrGlnAsnArgProLeuLeuArgAsnSerLeuAspAspLeuValGlyPro
ATGATGATGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCA
                                                 MetMetMet....
                                                                               lnArgSerArgGluLeuLeuSerHisHisPheArgGlnGlnArgValAla
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                                                                                                                                                                                                                                                                                                                            lyGlyPheHisLeuGlnGlyGlnSerProSerPheAsnSerMetMetAsn
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                                                 .GlnGlnGlnGlnGlnGlnGlnGlnGl 1253
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APPLICANT: Shyjan, Andrew W.
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USE
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.1183-001
CURRENT APPLICATION NUMBER: US/09/652,127
CURRENT FILING DATE: 2000-08-30
PRIOR APPLICATION NUMBER: 60/151,134
PRIOR FILING DATE: 1999-08-30
NUMBER OF SEQ ID NOS: 10475
SOSTWARE: FastSEQ for Mindows Version 4.0
SEQ ID NO 9831
LENGTH: 7888
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; ORGANISM: Homo
US-09-652-127-9831
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                                                                                                                                                 Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 9831, Application US/09652127 GENERAL INFORMATION:
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AsnGlySerSerGlyHisMetGlyGlnMetAsnMetAsnProMetProMe 1403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               erSerProProAsnAlaMetMetSerSerArgMetGlyProSerGlnAsn 1336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nProAsnTyrGlyMetGlyGlnGlnProAspProAlaPheGlyArgValS 1320
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97.831
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lyHisLysLysLeuLeuGlnL 624	.uSerSerValGluGlyAlaG1 607 	MetCysGlnSerAsnSerArg 590 	erLysSerProLeuGlyPheT 574 	nSerProAsnMetAsnIleTh 557 	GlyThrSerLeuLeuSerThr 540 	erPheSerSerSerSerLeuS 524	llAlaGlyValHisSerProme 507 	ProArgAsnArgGlySerPro 490	roHisGlySerProGlyLeuA 474 	irProSerSerTyrGlnAsnAs 457 	GlyGlySerSerAsnIleAla 440	YrGlyLeuAlaAspProSerT 424 	yMetSerMetSerProAsnGl 407 	.GlyGlnGlyIleArgProPro 390 	isPheLeuGlnArgGluGlnA 374 	'sLeuPheArgAsnProValTh 357 	ArgPheSerLeuAlaAspGly 340	NTATTTTCCCCAACAGCTTATC 1181

907	891 2882	87 4 2832	857 2782	841 2732	824 2682	807 2632	791 2582	774 2532	757 2482	741 2432	724 2382	707 2332	691 2282	674 2232	657 2182	641 2132	624 2082	2032
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ThrProSer	snTyrGlyS ATTATGGCT	oLysGlnPr !AAAGCAACC	ValGlySer GTTGGCTCA	SerIleArgP CTATTCGTC	IPheGlnGl GTTTCAAGG	AsnAsnSer !AATAATTCC	euAspAsnL TGGATAATC	luLysAspPr \GAAAGACCC	AsnLysMet AATAAAATG	roSerAspA CTAGTGATG	SLYSLYSG1 GAAGAAGGA	ThrSerCys	luValAlaL AGGTAGCCA	uLysHisAr GAAGCACCG	SerGlyGly TCTGGAGGA	ysGluSerS AAGAATCTT	PASPArgG1 TGACCGGGG	
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uProA	AsnAr	roArg CAAGA	nIleS TATCA	Valse GTGTC	euLys TGAAA	rHisL TCATC	AspLe GATCT	hrser CAAGT	rThrI	GlnPr CAGCC	rgTyr GATAC	lLysg CAAGC	ThrG1 ACTGG	euGln TGCAG	nMetH TATGC	ProSe CCCTC	snSer ACTCC	 GCAGT
924	907 2917	890 2881	874 2831	857 2781	840 2731	82 4 2681	807 2631	790 2581	774 2531	757 2481	740 2431	724 2381	707 2331	690 2281	674 2231	657 2181	640 2131	2081

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1190	euGlnGlnArgLeuGlnGlyGlnGlnPheLeuAsnGlnSerArgGlnAla	1174
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3686		3637
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3586		3537
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3136		3087
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957 3036	ProGlyGlyAspTyrAsnThrSerLeuProArgProAlaLeuGlyGlySe	· 941 2987
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2986		2937
2936		2918

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Quality:
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; GENERAL INFORMATION:
                                                           NUMBER OF SEQ ID NOS:
SOFTWARE: FASTSEQ for
SEQ ID NO 11058
LENGTH: 7888
TYPE: DNA
ORGANISM: Homo sapiens
US-09-652-355-11058
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                                                                                                                                                                        APPLICANT: Shyjan, Andrew W.
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOTTLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.1192-001
CURRENT APPLICATION NUMBER: US/09/652,355
CURRENT FILING DATE: 2000-08-30
PRIOR APPLICATION NUMBER: 60/151,136
PRIOR FILING DATE: 1999-08-30
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507 talaserSerGlyAsnThrGlyAsnHisSerPheSerSerSerLeuS 524	1582 CAACTATAGGCTCAACATGAGTAGCCCCCAACATGGGAGTCCTGGTCTTG 1631 474 laProAsnGlnGlnAsnIleMetIleSerProArgAsnArgGlySerPro 490	424 hrThrGlyGlnMetSerGlyAlaArgTyrGlyGlySerSerAsnIleAla 440	MetAlaGlyCysAsnSerSerValGlyGlyMetSerMetSerProAsnGl	341 ThrILeValThralaGlnThrLysSerLysLeuPheArgAsnbroValTh 357	ATTCAGAGATTTTTTAGTCTAAATGATGGCAGTCATGGTCCCAGAAACG gHisTyrGlnGlu	
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GlnMetAsnGlnGlnGlyAsnPheProLeuGlnGlyMetHisProArgAl
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.seq:US-09-663-693-1028
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seq_documentation_block:

Sequence 1028, Application US/09663693

GENERAL INFORMATION:
APPLICANT: GEARING, David P.
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.1195-001
CURRENT APPLICATION NUMBER: US/09/663,693
CURRENT FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: 60/154,986
PRIOR APPLICATION NUMBER: 60/154,986

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SOFTWARE: FastSEQ for Wi
SEQ ID NO 1028
LENGTH: 7888
TYPE: DNA
ORGANISM: Homo sapiens
US-09-663-693-1028
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Quality: 7233.50
Ratio: 5.174
Percent Similarity: 97.831
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SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                           hrAsnGluProGlnArgGlnLysSerHisThrPheAsnCysArgMetLeu
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|CAAATGAGACCCAAAGACAAAAAAGCCATACATTTAATTGCCGTATGTTG
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Gaps:
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490 168	474 laProAsnGlnGlnAsnIleMetIleSerProArgAsnArgGlySerPro	
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457 158	441 SerLeuThrProGlyProGlyMetGlnSerProSerSerTyrGlnAsnAs	
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324 118	317 9H1STYTGLnGluAlaTYTL + + + + + + + 1132 TCACTATCAAGAAGTTACCAGTGATGGGATATTTTCCCCCAACAGCTTATC	
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                                                            AsnGlySerSerGlyHisMetGlyGlnMetAsnMetAsnProMetProMe
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seq_name:

/cgn2_6/ptodata/1/pna/US096E_COMB.seq:US-09-698-014-5135

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Sequence 5135, Application US/09698014

GENERAL INFORMATION:
APPLICANT: Gearing, David P.
APPLICANT: Holtzman, Douglas A.
APPLICANT: Kingsbury, Gillian A.
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES ANT TITLE OF INVENTION: THEREFOR FILE REFERENCE: 1600.2014-001

CURRENT APPLICATION NUMBER: US/09/698,014

CURRENT FILING DATE: 2000-10-27

PRIOR APPLICATION NUMBER: 60/162,363

PRIOR FILING DATE: 1999-10-29

NUMBER OF SEQ ID NOS: 6098

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 5135

LENCTH: 7888
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; Sequence 5135, Applica
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_block:
US-09-041-994-2 x US-09-698-014-5135
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    Quality:
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US-09-698-014-5135
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PETGLIAGAATTTACCAAAATCCTACCATTCCTCCAAACGCTATATCCTACAATTTACCAAAAACCCCAAAGACAAAAAAACCCCAAAGACAAAAAA	ThrG1	tAlaG	TILEV TATAG TATAG SnAsp GLYTY GLYTY GGATA	idsTyr ACTAT ASnG1 	TTACC LeuAr CTGAG 	gArgI CCGCA	rgGln GCCAG MetMe	AsnGl AATGA tLysT 	HILL
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757 oGlnVal	741 LeuLeuA 11 2432 CTGCTGG	724 lnGluGli 2382 AGGAGCA	707 yLysAsp 2332 GAAAGAC	691 AsnGlyA: 11 2282 AATGGGA	674 isGlySe 11 2232 ATGGGTC	657 rGlyVal	641 ProLeuA 2132 CCCCTAG	624 euLeuTh 1111 2082 TACTTAC	607 uAsnGln 11 2032 GAATCAA	591 AspHisL	574 yrCysAs 1932 ATTGCGA	557 rGlnPro 1882 CCAACCA	541 LeuSerS 1832 CTGTCAT	524 erAlaLe 1782 GTGCCCT	507 tAlaSer 1732 GGCATCT	491 LysileA 1682 AAGATAG	474 laProAs 1632 CCCCAAA	1582 СААСТАТ
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774 2531	757 2481	740 2431	724 2381	707 2331	690 2281	674 2231	657 2181	640 2131	6 24 2081	607 2031	590 1981	574 1931	557 1881	540 1831	524 1781	507 1731	490 1681	1631

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```
Sequence 7321, Application US/09716475

GENERAL INFORMATION:
APPLICANT: Shyjan, Andrew W.
APPLICANT: Washeth, Kyle J.
APPLICANT: Washeth, Myle J.
APPLICANT: Washeth, Myle J.
APPLICANTON. INFORMATION ACTION AND ACT OF INVESTION AND ACT OF INVESTION APPLICATION NUMBER: US/09/716,475
CURRENT FILING DATE: 2007-11-20
PRIOR APPLICATION NUMBER: 60/166,506
PRIOR FILING DATE: 1999-11-19
NUMBER OF SEQ ID NOS: 8194
SOFTWARE: FASTSEQ FOR WINDOWS VETSION 4.0
SEQ ID NO 7321
LENGTH: 7888
TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: /cgn2_6/ptodata/1/pna/US097A_COMB.seq:US-09-716-475-7321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: US-09-716-475-7321 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-041-994-2 x US-09-716-475-7321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality: 7233.50
Ratio: 5.174
Percent Similarity: 97.831
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           282 AAAAACGGAGACGGAGCAGGAAAGTAAATATATTGAAGAATTGGCTGAG
                                                                                                                                                                                                                                                                                                                                                                            232 ACGCAAATTGCCATGTGATACTCCAGGACAAGGTCTTACCTGCAGTGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                   182 ATGAGTGGATTAGGAGAAAACTTGGATCCACTGGCCAGTGATTCACGAAA 231
                                                                                                                                                                                                                                                                                                                     34 luLysArgArgArgGluGlnGluSerLysTyrIleGluGluLeuAlaGlu
                                                                                                                                                                                                                                                                                                                                                                                             17 sArgLysLeuProCysAspThrProGlyGlnGlyLeuThrCysSerGlyG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MetSerGlyLeuGlyGluAsnLeuAspProLeuAlaSerAspSerArgLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Identity: 97.621
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N	7 nGlyLeuGlnMetProSerSerArgAlaTyrGlyLeuAlaAspProSerT	4
407 1431	1 MetAlaGlyCysAsnSerSerValGlyGlyMetSerMetSerProAsnGl	39 138
390	4 snGlyTyrArgProAsnProAsnProValGlyGlnGlyIleArgProPro	37
1381		133
374	7 rasnaspargHisGlyPheValSerThrHisPheLeuGlnargGluGlna	35
1331		128
357	1 ThrileValThralaGlnThrLysSerLysLeuPheArgAsnProValTh	34
1281		123
340	4 euAsnGlyHisAlaGluThrProValTyrArgPheSerLeuAlaAspGly	32
1231		118
324 1181	7 9HisTyrGlnGluAlaTyrL 2 TCACTATCAAGAAGTTACCAGTGATGGGATATTTTCCCCAACAGCTTATC	31 113
317	1 IleGlnArgPhePheSerLeuAsnAspGlyGlnSerTrpSerGlnLysAr	30
1131		108
300	4 erLeuArgSerSerMetArgProGlyPheGluAspIleIleArgArgCys	28
1081		103
284	57 eIleThrargHisaspLeuSerGlyLysValValasnTleaspThrasnS	26
1031		98
267	1 ArgargIleThrThrGlyGluArgThrPhe	93
981		93
250	4 lametmetGluGluGlyGluAspLeuGlnSerCysMetI	23
931		88
234	7 targGlnArgTyrGluThrMetGlnCysPh	21
881		83
217 831	1 MetLysThrProHisAspIleLeuGluAspIleAs 	
200 781	4 hrasnGluProGlnArgGlnLysSerHisThrPheAs	18 73
184	7 sAspPheLeuLysAsnLeuProLysSerThrValAsnG1	16
731		68
167 681	AspLeuValAsnThrSerVal	15 63
150	4 leValPheValSerGluAsn	13
631		58
581	ACTTCAGGCATTGGATGGTTTCCTAT	532

707	J 7	N O	657 rGlyValSerSerShrSerGlyGlyValSerSerThrSerAsnMetH 674	641 ProLeuAspSerSerCysLysGluSerSerValSerValThrSerProSe 657	624 euLeuThrCysSerSerAspAspArgGlyHisSerSerLeuThrAsnSer 640 	607 uAsnGlnArgGlyProLeuGluSerLysGlyHisLysLysLeuLeuGlnL 624 	591 ASPHISLeuSerAspLySGluSerLySGluSerSerValGluGlyAlaGl 607 	574 yrcysAspGlnAsnProValGluSerSerMetCysGlnSerAsnSerArg 590 	557 rGlnProSerLysValSerAsnGlnAspSerLysSerProLeuGlyPheT 574 	541 LeuSerSerProGlyProLysLeuAspAsnSerProAsnMetAsnIleTh 557 	524 eralaLeuGlnAlaIleSerGluGlyValGlyThrSerLeuLeuSerThr 540 	507 tAlaSerSerGlyAsnThrGlyAsnHisSerPheSerSerSerLeuS 524 	491 LysIleAlaSerHisGlnPheSerProValAlaGlyValHisSerProMe 507 	474 laProAsnGlnGlnAsnIleMetIleSerProArgAsnArgGlySerPro 490 	nAsnTyrGlyLeuAsnMetSerSerProProHisGlySerProGlyLeuA 	441 SerLeuThrProGlyProGlyMetGlnSerProSerSerTyrGlnAsnAs 457 	44 15	
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1007 uGlySerTrpProAspGlyMetLeuSerMetGluGlnValSerHisGlyT 1024 	991 MetGlyMetGlyAlaAsnProTyrGlyGlnAlaAlaAlaSerAsnGlnLe 1007 	974 alLeuGlnGlnGlnGlnGlnMetLeuGlnMetArgProGlyGluIlePro 990	3037 TATTCCCACATTGCCTCTTCGGTCTAATAGCATACCAGGTGCGAGACCAG 3086	Prod.lyG1yAspTyrAsnThrSerLeuProArgProAlaLeuG1yG1ySe 	SIDSETLYSALAG_YATGMEGILUFTOMECASIDSETASIDSETMEGIJYATG	gAsnValThrValThrGlnThrProSerSerGlyAspTrpGlyLouProA		ERALAPHEPTOMELLEUPTOLÝSULHPTOMECLEUGIÝGLÝASHIPTOATG	T-GuASpSerProValSerValGlySerSerProProValLySasnIleS	1 SerSercinSerValGinSerIleArgProProTyrAsnArgAlaValSe	euG1yThrTysG.InG1NVa1PheG1nG1yThrAsnSerLeuG1yLeuLys 	uThrSerSerAsgPheTyrAsnAsnSerIleSerSerAsnGlySerHisL 	GluGluGlySerGlyAspLeuAspAsnLeuAspAlaIleLeuGlyAspLe 	LeProSerSerSerGInGLuLysAspProLysILeLysThrGluThrSer 	OGlnValGluGlyValAspAsnLysMetSerGlnCysThrSerSerThrI	741 LeuLeuAspArgAspAspProSerAspAlaLeuSerLysGluLeuGlnPr 757	724 IngluGlnLeuSerProLysLysLysGluAsnAsnAlaLeuLeuArgTyr 740 	2332 GAAAGACACCAGCAGTATAACTTCTTGTGGGGACGGAAATGTTGTCAAGC 2381

1320	nProAsnTyrGlyMetGlyGlnGlnProAspProAlaPheGlyArgValS	1303
4136		4087
1303	LeuAlaGlyProThrMetProGlnAlaProProGlnGlnPheProTyrGl	1287
4086		4037
1286	laPheSerProProProAsnValThrAlaSerProSerMetAspGlyLeu	1270
4036		3987
1270 3986	nGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln	1253 3937
1253	MetMetMetGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGl	1241
3936		3887
1240 3886	0-5	1224 3837
1224 3836	gPrometMetGlnProGlnGlnGlyPheLeuAsnAlaGlnMetValAlaG	1207 3787
1207	LeuGluLeuLysMetGluAsnProThrAlaGlyGlyAlaAlaValMetAr	1191
3786		3737
1190 3736	euGlnGlnArgLeuGlnGlyGlnGlnPheLeuAsnGlnSerArgGlnAla	1174 3687
1174	aAsnIleMetArgProArgThrAsnThrProLysGlnLeuArgMetGlnL	1157
3686		3637
1157 3636	GlnMetAsnGlnGlnGlyAsnPheProLeuGlnGlyMetHisProArgAl	1141 3587
1140	1yG1yPheHisLeuGlnG1yG1nSerProSerPheAsnSerMetMetAsn	1124
3586		3537
1124	salaGlyLeuTyrGlyGlnThrTyrProalaGlnGlyProProMetGlnG	1107
3536		3487
1107 3486	LygGlnAgpAlaPheGlnGlyGlnGluAlaAlaValMetMetAspGlnLy	1091 3437
1090	rgAlaLeuGlyIleProGluLeuValAsnGlnGlyGlnAlaLeuGluPro	1074
3436		3387
1074	uHisThrLeuLeuSerAsnThrAspAlaThrGlyLeuGluGluIleAspA	1057
3386		3337
1057 3336	ProSerAsnLeuGluGlyGlnSerAspGluArgAlaLeuLeuAspGlnLe	1041 3287
1040	hrGlnAsnArgProLeuLeuArgAsnSerLeuAspAspLeuValGlyPro	1024
3286		3237

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Sequence Sequence Sequence Compact Secure Left | Documentation | A | Secure Sequence | Secure Left | Documentation | A | Secure Sequence | Secure Left | Documentation | A | Secure Sequence | Sequenc
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Query length: 1415
Database: Pending_Patents_NA_New:*
Database sequences: 201016
Database length: 146721182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OM of: US-09-041-994-2 to: Pending_Patents_NA_New:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -MODEL=frame+_p2n.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool/US09041994/runat_30042001_165632_19523/app_query.fasta_1.1940
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-DB=Pending_Patents_NA_New -CPMT=fastap -SUFETX=p2n.rnpn
-GAPOP=12.000 -GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000
-LOOPEXT=0.000 -GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000
-YGAPEXT=0.500 -GAPEXT=6.000 -GAPEXT=7.000 -YGAPOP=10.000
-YGAPEXT=0.500 -DELOP=6.000 -DELEXT=7.000 -YGAPOP=10.000
-YGAPEXT=0.500 -DELOP=6.000 -DELEXT=7.000 -YGAPOP=10.000
-YGAPEXT=0.500 -DELOP=6.000 -DELEXT=7.000 -YGAPOP=10.000
-YGAPEXT=0.500 -DELOP=6.000 -DELEXT=7.000 -YGAPOP=10.000
-YGAPEXT=0.500 -THR_MAX=100 -THR_MIN=0.7ALIGN=15 -MODE-LOCAL
-UNITALISHED - MAXLEN=200000000
-USER=US09041994_@CGN1_1_175 -NCPU=6 -ICPU=3 -LONGLOG -NO_XLPXY
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                                            :US-09-543-679A-2717 + 184.00
:US-09-543-679A-2752 + 184.00
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                                                                                134
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alignment_block:
US-09-041-994-2 x US-09-196-296B-1
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Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: Homo
US-09-196-296B-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
; Sequence 1, Application
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:US-09-335-032-12215 + 182.50 115.74 /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq:US-09-139-5749 + 181.00 156.98 /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq:PCT-US01-01339-9949 - 181.00 156.98 /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq:PCT-US01-08117-122 + 181.00 153.74 (cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq:PCT-US01-08117-122 + 181.00 153.74 (cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq:US-60-248-505-39 + 181.00 143.25 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/196,296B
CURRENT FILING DATE: 1998-11-19
NUMBER OF SEQ ID NOS: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Suen, Chen-Shian
APPLICANT: Frail, Donald E.
APPLICANT: Lyttle, Richard C.
TITLE OF INVENTION: Cloning and Expression of a Nuclear
TITLE OF INVENTION: Receptor Coactivator Proteins and FILE REFERENCE: 0630/01376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84 luGlnGlyLysThrIleSerAsnAspAspAspYalGlnLysAlaAspYal 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51 LeuIleSerAlaAsnLeuSerAspIleAspAsnPheAsnValLysProAs
                                                                                                                                                                 SerSerThrGlyGlnGlyValIleAspLysAspSerLeuGlyProLeuLe
leValPheValSerGluAsnValThrGlnTyrLeuGlnTyrLysGlnGlu 150
                                                                              pLysCysAlaIleLeuLysGluThrValArgGlnIleArgGlnIleLysG
                                                                                                                                            TCTTCTACAGGGCAGGGAGTTATTGATAAAGACTCCTTAGGACCGCTTTT
                                                                                                                                                                                                                           AGCAAGGAAAAACTATTTCCAATGATGATGATGTTCAAAAAGCCGATGTA
                                                                                                                                                                                                                                                                                                           TAAATGTGCGATTTTAAAGGAAACAGTAAGACAGATACGTCAAATAAAAG
                                                                                                                                                                                                                                                                                                                                                                                            CTGATATCTGCCAATCTTAGTGATATTGACAATTTCAATGTCAAACCAGA
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GGGGAAGATTTTGCAATCTTGTATATCTGTTGGGAGGAAGATTTGCAATCTGTTTGGCATCTGTTGGGATGGTTGGGATGGGAAGATTTGCAATCTGTTTGGATTTGGCATCTGTTGGGATGGCTGGAAAAAAAA	
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GlyGluAspLeuGlnSerCysMetIleCysV	234 laMetMetGluGlu
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16		1585
14 G	ProSerSerTyrGlnAsnAsnAsnTyrGlyLeuAsnMetSerSerProPr 	451 1535

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; SEQ ID NO 3; LENGTH: 3361; TYPE: DNA; ORGANISM: Murine US-09-196-296B-3
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Sequence 3, Application US/09196296B
GENERAL INFORMATION:
APPLICANT: Suen, Chen-Shian
APPLICANT: Frail, Donald E.
APPLICANT: Lyttle, Richard C.
APPLICANT: Lyttle, Richard C.
TITLE OF INVENTION: Receptor Coactivator Proteins and Uses Thereof
FILE REFERENCE: 0630/01376
CURRENT APPLICATION NUMBER: US/09/196,296B
CURRENT FILING DATE: 1998-11-19
NUMBER OF SEQ ID NOS: 3
SOFTWARE: FastSEQ for Windows Version 3.0
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US-09-041-994-2 x US-09-196-296B-3
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Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
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|||||||||||||||||
|TCCTGATCAGAAATACTGC 4453
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2.840
23.087
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Gaps: 4
Percent Identity: 21.585
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2153

and

Antibodies

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; SEQ ID NO 9844
; LENGTH: 24387
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-USO1-01339-9844
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Quality:
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Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 9844, Application PC/TUS0101339
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc., et al
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PC006PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: PCT/US01/01339 CURRENT FILING DATE: 2001-03-17
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Percent Identity:
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us-09-041-994-2.p2n.rnpn

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Human Genome Sciences, Inc., et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC006CCT
CURRENT APPLICATION NUMBER: PCT/US01/01339
CURRENT FILING DATE: 2001-03-17
NUMBER OF SEQ ID NOS: 10231
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7281
LENGTH: 13555
TYPE: DNA
ORGANISM: Homo Sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11003 AAAAATCGAGGTCTTCACGCCGACGGCGCTCAGCTTCATCTCCACGCACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11191 ATCACCAGAGCCCAAGACCAAGTCTCGTACACCACCT......
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1316 ......PheGlyArgValSerSerProProAsnAla 1325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1299 nPheProTyrGlnProAsnTyrGlyMetGlyGlnGlnProAspProAla. 1315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1255 nGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnThrGlnAlaPheS 1272
                                                                                                                                                                                                                                                                                           5108 TCCCCTCAAGTCAAAGATACCACCATTTCCTCAGTTCTGATTTCTCCACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1239 ValAlaMetMetGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGl 1255
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                                                                                                                                                                                                                                                                                                                                                  330 ThrProValTyrArgPheSerLeuAlaAspGlyThrIleValThrAlaGl 346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTG.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MetMetSerSerArgMetGlyProSerGlnAsnPro 1337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality:
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44.060
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6916	TO THE THAT IT YET YET SET ME COT YET YET YET OF THE COT	6965
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8269	GGCCCCCACT	8220
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Sequence 12207, Application US/09335032

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APPLICANY: Voyelstein, Bert
APPLICANY: Voyelstein, Bert
APPLICANY: Voyelstein, Characterization of the Yeast
TITLE OF INVENTION: Characterization of the Yeast
TITLE OF INVENTION: Transcriptome
FILE REFERENCE: 01107.78572
CURRENT APPLICATION NUMBER: US/09/335,032
CURRENT APPLICATION NUMBER: US 60/035,917
PRIOR APPLICATION NUMBER: US 60/035,917
PRIOR APPLICATION NUMBER: US 99/012,031
PRIOR FILING DATE: 1998-01-22
NUMBER OF SEQ ID NOS: 12219
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12207
LENGTH: 1531974
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Quality:
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; ORGANISM: Saccharomyces cerevisiae
US-09-335-032-12207
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254 hrThrGlyGluArgThrPheProSerAsnProGluSerPheIleThrArg 270
                                                                                                                                                                                                                                                          235 MetMetGluGluGlyGluAspLeuGlnSerCysMetIleCysValAlaAr 251
                                                                                                                                                                                                                                                                                                                                                    219 lnArgTyrGluThrMetGlnCysPheAla...LeuSerGlnProArgAla 234
::: |||||| ||| |||||||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   190 GlnLysSerHisThrPheAsnCys......ArgMetLeuMetLy 202
                                                                                                                                         251 gArgIle.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        202 sThrProHisAspIleLeuGluAspIleAsnAlaSerProGluMetArgG 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              226.00
0.400
43.495
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Gaps: 61
Percent Identity: 19.477
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                                                                                                                                               254
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525 1194125	509 erSerGlyAsnThrGlyAsnHisSerPheSerSerSerSerLeuSerAla ::::: ::: ::::: ::::::::::::::::
509 1194172	492 eAlaSerHisGlnPheSerProValAlaGlyValHisSerProMetAlaS
1194215	1194215
492	476 AsnGlnGlnAsnIleMetIleSerProArgAsnArgGlySerProLysIl
475 1194215	459 yrGlyLeuAsnMetSerSerProProHisGlySerProGlyLeuAlaPro
459 1194265	442 uThrProGlyProGlyMetGlnSerProSerSerTyrGlnAsnAsnAsnT :::
442 1194315	426 GlyGlnmetSerGlyAlaArgTyrGlyGlySerSerAsnIleAlaSerLe
425 1194362	409 euGlnMetProSerSerArgAlaTyrGlyLeuAlaAspProSerThrThr ::: 1194369AGAAGATG
409 1194370	392 aGlyCysAsnSerSerValGlyGlyMetSerMetSerProAsnGlnGlyL:::: ::::: :::: :::::
392 1194413	387 IleargProProMetal :::
386 1194461	370 lnArgGluGlnAsnGlyTyrArgProAsnProAsnProValGlyGlnGly :::::: :::
370 1194502	355 OValThrAsnaspArgHisGlyPheValSerThrHisPheLeuG ::::: :::: ::::
355 1194552	343 ValThrAlaGlnThrLysSerLysLeuPheArgAsnPr ::::::::::::::::::::::::::::::::::::
342 1194602	328AlaGluThrProValTyrArgPheSerLeuAlaAspGlyThrIle ::: :::
1194652	1194701TATACGAAGGGGTATAAGGTTTGACGAGGCGTCACTGCCGAAGCTCCTAC
327	327
327 1194702	312 SerTrpSerGlnLysArgHisTyrGlnGluAlaTyrLeuAsnGlyHis ::: ::: ::: ::: ::: 1194751GATGAAAACAAACTTCGGAAGGAAATAGATGCATTTTTAAAGAAAAACGA
311 1194752	300CyslleGlnArgPhePheSerLeuAsnAspGlyGln ::::: ::: 1194801TGACCGAACTATACTGCGTATCCCGCTTGAACCAGCTGCTAGAGTTAACA
299 1194802	287 rSerMetArgProGlyPheGluAspIleIleArgArg
287 1194849	271 HisaspLeuSerGlyLysValValAsnIleAspThrAsnSerLeuArgSe ::::::: :::
1194890	1194936CAGTTTCCGCCTCAAAGATGTCCTCACGTCCAAGTTCAGCAGTGCCT

526 LeuGlnAlaIleSerGluGlyValGlyThrSerLeuLeuSerThrLeuSe	542
	1194104
SLeuAspAsnSerProAsnMetAsnIleThrGlnP	559 1194088
.nAspSerLysSerProLeuGlyPheTyrCys ::: ::: !TTTGCCCTTAGCAGAATTGAAGTACATGTCA	575 1194038
576 AspGlnAsnProValGluSerSerMetCysGlnSerAsnSerArgAspHi :::	592
	1194026
rLysGluSerSerValGluGlyAlaGluAsnG	609
194026	1194026
yProLeuGluSerLysGlyHisLysLysLysLeuLeuGlnLeuLeu :::: ::: 	625 1194011
SerSerAspAspArgGlyHisSerSerLeuThrasnSerProLe ::: ::: ::: ::::: 	642 1193976
CysLysGluSerSerValSerValThrSerProSerGlyV::: ::: ::	659 1193929
659 alserSerSerThrSerGlyGlyValSerSer	669 1193879
670ThrSerAsnMetHisGlySerLeuLeuGlnGl	680 1193829
680 uLysHisArgIleLeuHisLysLeuLeuGlnAsnGlyAsnSerProAlaG ::: :::::::::::::::::::::::::::::::	697 1193782
697 luvalalaLysIleThrAlaGlnAlaThrGlyLysAspThrSerSer 	712 1193741
713 IleThrSerCysGlyAspGlyAsnValValLysGlnGluGlnLeuSerPr ::: :::	729 1193691
729 OLYSLYSGIUASNASNAIaLeuLeuArgTyrLeuLeuAspArgAspA 	746 1193665
746 sp	753 1193615
alGluGlyValAspAsn	765 1193565
765 sMetSerGlnCysThrSerSerThrIleProSerSerGlnGluLysA	782 1193542
782 spProLysIleLysThrGluThrSerGluGluGly	793 1193492

1093	1077 GlvIleProGluLeuValAsnGlnGlvGlnAlaLeuGluProLvsGlnAs
1076 1192766	1060 euLeuSerAsnThrAspAlaThrGlyLeuGluGluIleAspArgAlaLeu :::::: :::
1060 1192804	1046GlyGlnSerAspGluargAlaLeuLeuAspGlnLeuHisThrL
1045 1192848	1031 ArgAsnSerLeuAspAspLeuValGlyProProSerAsnLeuGlu
1030 1192877	1014 etLeuSerMetGluGlnValSerHisGlyThrGlnAsnArgProLeuLeu
1014	997 oTyrGlyGlnAlaAlaAlaSerAsnGlnLeuGlySerTrpProAspGlyM 192928ATATGGCTACAATTGGAATTGG
997 1192929	981 MetLeuGlnMetArgProGlyGluIleProMetGlyMetGlyAlaAsnPr
980 1192979	964 rgSerAsnSerIleProGlyAlaArgProValLeuGlnGlnGlnGlnGln
964 1193026	947 rSerLeuProArgProAlaLeuGlyGlySerIleProThrLeuProLeuA ::: 3050GGTAATAGAAGAAATCATTATTTAA
947 1193051	931 GluProMetAsnSerAsnSerMetGlyArgProGlyGlyAspTyrAsnTh
930 1193096	914 hrProSerSerGlyAspTrpGlyLeuProAsnSerLysAlaGlyArgMet :::::: :::: ::: 1193145TGGATGATAGTGATTTTATAAGTTACTTGAGCGTCAATTGATTG
914 1193146	897 nTyrGlySerSerMetGlyGlyProAsnArgAsnValThrValThrGlnT
897 1193175	885 LeuGlyGlysnProargMetMetAspSerGlnGluAs ::: ::: 1193224TATAATGGTATTAATGAAGAACGGCCAAAAAAAGATGATTCTTTACCATT
884 1193225	868 roProValLysAsnIleSerAlaPheProMetLeuProLysGlnProMet
868 1193267	851 oTyrAsnArgAlaValSerLeuAspSerProValSerValGlySerSerP
851 1193295	835 AsnSerLeuGlyLeuLysSerSerGlnSerValGlnSerIleArgProPr :::::: :::::::::::::: :::::::
834 1193342	819SerAsnGlySerHisLeuGlyThrLysGlnGlnValPheGlnGlyThr :::::: ::::: 1193391CATCCTCCTCAAGCGAAGTTGTTTTAATACAACATGAAGTAGCTGCATCA
818 1193392	809 rSerAspPheTyrAsnAsnSerIleSer
809 1193442	794SerGlyAspLeuAspAsnLeuAspAlaIleLeuGlyAspLeuThrSe ::::: ::: :::: ::: 1193491GCTAAGAGTGATTTTGATTTTGCAGATGGTTTGTTATCTCAAGAAGGTGC

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1192337TCCAAGACCA.....AACCAGAAACAGTATACTGAGCAAGATATCA 1192297
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                                                                                1192005CCACAGGAGATTTTACAAAGGTTCCAAAAACAATGACCTAACTTT 1191961
                                                                                                                                                                                                                                  1192052CCAATATTTCTAACATTAATTCTGCTCCAAGGATAAAGTCACCAACT...
                                                                                                                                                                                                                                                                                                                                                                                        1192096TCAAGCTCCGCCACAAA.....TCATCTCCATCTCAATCTTCTTT 1192053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1192196ACAGCAACAGCTAAAGCAGCACCAGATTCAACAGCAAAGGCAGCAGTTAC 1192147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1192246GAGATGGCCCTTAAGGCGGCAAAAAACTATTATAGAACCTTGAGAGAACA 1192197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1192296TTGAAAAGTTACTCGAGGAAGTTGTTGGAGCAAAAACCAGACATTGGTCCT 1192247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1192146AGGAGGAGTCCAGTCATGTGCAGCAACTGCAGCAACTACAACCAGGGTCT 1192097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1192387TCAAATGGCAAATCTTCTTCAAATTTGGCTAGAAATGGGCAAGCGTCGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1143 nGlnGlnGlyAsnPheProLeuGlnGlyMetHisProArgAlaAsnIleM 1160
                                                                                                                                 1293 ProGlnAlaProProGlnGlnPheProTyrGln...ProAsnTyr 1306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1271 PheSer.ProProProAsnValThrAlaSerProSerMetAspGlyLeu. 1286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1254 lnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnThrGlnAla 1270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1234 .....PheArgGlnGl 1237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1222 alAlaGlnArgSerArgGluLeuLeuSerHisHis.......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1205 lMetArgProMetMetGlnProGlnGlnGlyPheLeuAsnAlaGlnMetV 1222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1184 euAsnGlnSerArgGlnAlaLeuGluLeuLysMetGluAsnProThrAla 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1169 ....GlnLeuArgMetGlnLeuGlnGlnArgLeuGlnGlyGlnGlnPheL 1184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1127 HisLeuGlnGlyGlnSerProSerPheAsnSerMetAsnGlnMetAs 1143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1110 euTyrGlyGlnThrTyrProAlaGlnGlyProProMetGlnGlyGlyPhe 1126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1093 pAlaPheGinGlyGlnGluAlaAlaValMetMetAspGlnLysAlaGlyL 1110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:US-09-335-032-12216
                                                                                                                                                                                                                                                                                                               .....LeuAlaGlyProThrMet 1292
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APPLICANT: Velculescu, Victor
APPLICANT: Vogelstein, Bert
APPLICANT: Kinzler, Kenneth
APPLICANT: Kinzler, Kenneth
TITLE OF INVENTION: Characterization of the Yeast
TITLE OF INVENTION: Transcriptome
FILE REFERENCE: 01107.78572
CURRENT APPLICATION UNMBER: US/09/335,032
CURRENT FILING DATE: 1999-06-16
PRIOR APPLICATION NUMBER: US 60/035,917
PRIOR FILING DATE: 1997-01-23
PRIOR APPLICATION NUMBER: US 09/012,031
PRIOR APPLICATION NUMBER: US 09/012,031
PRIOR FILING DATE: 1998-01-22
NUMBER OF SEQ ID NOS: 12219
SOSTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12216
LENGTH: 924430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Saccharomyces cerevisiae US-09-335-032-12216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_block:
US-09-041-994-2 x US-09-335-032-12216/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to reverse of: US-09-335-032-12216 from: 1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          592258 ACCGAGGGTGAAGGT.....GAAGGTGAAAATGAAAATAAGAAGAA 592218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 12216, Application US/09335032 GENERAL INFORMATION:
                                                                                                                               591960 GTTACAAGCCAAACAAGAATATGATGCATGACACAGACATACAA..... 591917
                                                                                                                                                                                                                                                                        592010 TATACCCAGTAAACTTGATAACAATGGCGACTTACTACTAGACACTGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   592100 ACCACCAGATTCAGTTGAAGAGAGG.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  592144 GAAACTACAGGGTCGCTTTCT.....CCTACTGAATCCTCTACAACGAC 592101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            592194 CAGATTTTTTAGATATCAATGACACTGGAGATTCAGGCAGTAAAAATAGT 592145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    157 alTyr......AsnIleLeuHisGluGluAspArgLysAspPhe 169
                                                                                                                                                                                                                                                                                                                                    140 nValThrGlnTyrLeuGlnTyrLysGlnGluAspLeuValAsnThrSerV 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          124 PheLeuPheValValAsnArgGluAlaAsnIleValPheValSerGluAs 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                107 alileAspLysAspSerLeuGlyProLeuLeuGlnAlaLeuAspGly 123
                                                               170 LeuLysAsnLeuProLysSerThrValAsnGlyValSerTrpThrAsnGl 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74 GluThrValArgGlnIleArgGlnIleLysGluGlnGlyLysThrIleSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57 erAspIleAspAsnPheAsnValLysProAspLysCysAlaIleLeuLys 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40 nGluSerLysTyrIleGluGluLeuAlaGluLeuIleSerAlaAsnLeuS 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24 ThrProGlyGlnGlyLeuThrCysSerGlyGluLysArgArgArgGluGl 40
|||||||:::||| | |||:::
CTGAAGCAGTTGTTAAAGGACGAATTCGGTAATGATTCAGATATTTCCAG
                                                                                                                                                                                                                                                                                                                                                                                                           TTTCAGCAAAAACTAAACAAAAAACTCACTGAAATC......CA 592011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rAsnAspAspAspValGlnLysAlaAspValSerSerThrGlyGlnGlyV 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .....AAGCTTGTTGAGCAGCGTACAAAGAAC 592049
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0.319
43.235
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   591867
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4	59114	ACGATGGCTGCGTTAAGGCGGGAAGTAATACTAAAAAAAA	591193
	451		451
4	451 59119	erAsnIleAlaSerLeuThrProGlyProGlyMetGlnSerPro	437 591232
ω	437 59123	### BASPPROSETHTHTHTGLYGINMETSETGLYALAATGTYTGLYGLYSETS	420 591278
ý	420 59127	SerProAsnGlnGlyLeuGlnMetProSerSerArgAlaTyrGlyLeuAl :::::: ::: :::	404 591316
.7	59131		591317
	403	${\tt leArgProProMetAlaGlyCysAsnSerSerValGlyGlyMetSerMet}$	387
7	387 591317	nargGluGlnAsnGlyTyrArgProAsnProAsnProValGlyGlnGlyI : ::::: GATCTCCAGGAATGGCTAT	370 591335
õ	370 59133	AsnProValThrAsnAspArgHisGlyPheValSerThrHisPheLeuGl::: ::: ::: ATGATAGGAAAAGACTGGACGCACTTGGGTGTAGCCAAGTTATTTAGCGA	35 4 591385
6	353 59138	euAlaAspGlyThrIleValThrAlaGlnThrLysSerLysLeuPheArg :::::::::::::::::::::::::	337 591435
Ö	337 59143	nGluAlaTyrLeuAsnGlyHisAlaGluThrProValTyrArgPheSerL:::: :::: TTGGAGGTGGGATGTTCCAATTGTTATCAGTG	320 591467
Č	320 59146	PhePheSerLeuAsnaspGlyGlnSerTrpSerGlnLysArgHisTyrGl	304 591517
œ	303 59151	SerMetArgProGlyPheGluAspIleIleArgArgCysIleGlnArg :::::: ::: ::: TAAATTTAACTTATGGTGAAAATGATCTG	288 591546
.7	287 59154	LysValValAsnIleAspThrAsnSerLeuArgSer. ::::::::::::::::::::::::::::::::::::	276 591596
17	275 59159	PheIleThrArgHisAspLeuSerGly	267 591646
7	266 59164	laArgArgIleThrThrGlyGluArgThrPheProSerAsnProGluSer::::::::::::::::::::::::::::::::::::	250 591696
97	250 59169	<pre>galametmetGluGluGlyGluAspLeuGlnSerCysMetIleCysValA</pre>	233 591739
O	233 59174	MetargGlnArgTyrGluThrMetGlnCysPheAlaLeuSerGlnProAr 	217 591775
o o	216 59177	hrProHisAspIleLeuGluAspIleAsnAlaSerProGlu:: ::::: :: ::::: ATCCTTACGAGCACCTTACTGATTTATCTCCTCGAGGTACGCCTCCAACA	203 591825
ō -	203 59182	uProGlnArgGlnLysSerHisThrPheAsnCysArgMetLeuMetLysT::::::::::::::::::::::::::::::::::::	186 591866

1L 727	rSerSerIleThrSerCysGlyAspGlyAsnValValLysGlnGlnL	710
AC 590445	III:::I	590452
rh 710	Asp	694
590453		590453
n 693	euLeuGlnGluLysHisArgIleLeuHisLysLeuLeuGlnAsnGlyAsn	677
. 590453	TTCCCATAGTAGCTCAGGATCCACGCCCAAT	590483
L 677	S	660
		590488
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              588299 ACTACAGCAA...
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                      APPLICANT: Velculescu, Victor
APPLICANT: Vogelstein, Bert
APPLICANT: Kinzler, Kenneth
TITLE OF INVENTION: Characterization of the
TITLE OF INVENTION: Transcriptome
FILE REFERENCE: 01107.78572
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                                                                                                                                                                                                                                                                                                                                                                                                    1389 erSerGlyHisMetGlyGlnMetAsn 1397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           eAlaHisGlnGlyAsnProAlaValTyrSerMetValHisMetAsnGlyS 1389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gly.....AsnLeuAlaArgAsnSerSerPheSerGlnGlnGlnPh 1372
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CURRENT FILING DATE: 1999-06-16
PRIOR APPLICATION NUMBER: US 60/035,917
PRIOR FILING DATE: 1997-01-23
PRIOR APPLICATION NUMBER: US 09/012,031
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PRIOR FILING DATE: 1998-01-22
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SEQ ID NO 12217
LENGTH: 784328
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US-09-335-032-12217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  526415 ACATTTAGAACATATCGGCTCTGTTTCATCAACTAATAAT...... 526454
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                526218 TCTCCGCTACACAGG...GAAATAGTTGATGATTCTGTCGCTACTGCTAA 526264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 427
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    456 snAsnAsnTyrGlyLeuAsnMetSerSerProProHisGlySerProGly 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    346 nThrLysSerLysLeuPheArgAsnProValThrAsnAspArgHisGlyP 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    330 ThrProValTyrArgPheSerLeuAlaAspGlyThrIleValThrAlaGl 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            410 lnMetProSerSerArgAlaTyrGlyLeuAlaAspProSerThrThrGly 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          380 ProAsnProValGlyGlnGlyIleArgPro.....ProMetAlaGl
523 LeuSerAlaLeuGlnAlaIleSerGluGlyValGlyThrSerLeu.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GlnMetSerGlyAlaArgTyrGlyGlySerSerAsnIleAlaSerLeuTh 443
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                                                                                                              roMetAlaSerSerGlyAsnThrGlyAsnHisSerPheSerSerSerSer
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0.436
52.681
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804 527652	rGluThrSerGluGluGlySerGlyAspLeuAspAsnLeuAspAlaIleL:::: :::: TTCAAGACATATTAGCACTGGTGCCATATTGAATAACACAA	787 527612
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1089 luProLysGlnAspAlaPheGlnGlyGlnGluAlaAlaValMetMetAsp 1105
                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTTAAGAATGAAACGTGGTCAAAGACACCTATCAAGAACAACAATAGC 528707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GlnLysAlaGlyLeuTyrGlyGlnThrTyrProAlaGlnGlyProProMe 1122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Leu 1191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lnGlnArgLeu...GlnGlyGlnGlnPheLeuAsnGlnSerArgGlnAla 1190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AATATCCGATTATGGTGAAGATGAAGACGTAGATGATTATGATCGCCCAA 528507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTCCAGAAGATAACGAAAGTGATGAAAACGATATTCACTCCATGTTT... 528419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      eAspArgAlaLeuGlyIleProGluLeuValAsnGlnGlyGlnAlaLeuG 1089
  FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                            PRIOR APPLICATION DATA: 60/009,861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Michael R. Fannon TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and NUMBER OF SEQUENCES: 5255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATA 528710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .IleMetArgProArgThrAsnThrProLysGlnLeuArgMetGlnLeuG 1175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCATTACATGGAAGGATGCCTTCAAGATCAAATAATGATTACTACGATTT 528607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          erProSerPheAsnSerMetMetAsnGlnMetAsnGlnGlnGlyAsnPhe 1148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tGlnGlyGlyPhe.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Charles Kunsch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .....TATTATAATCATAAGAACGATTTAGAAACAAAACCGCT 528457
                                                                                                                                          APPLICATION NUMBER: US/08/956,171C FILING DATE: 20-Oct-1997 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Human Genome Sciences, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Application US/08956171C
                                                                                                                                                                                                                                                                                                                                                           20850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gil H. Choi
Patrick S. Dillon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craig A. Rosen
Steven C. Barash
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ......HisLeuGlnGlyGlnS 1132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_block:
US-09-041-994-2 x US-08-956-171C-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE DESCRIPTION: SEQ ID NO: US-08-956-171C-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: US-08-956-171C-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                            20527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20239 ACAAGCGCAAAATGTAGCAGGTGTAAATGGTGTTAAAGATAAAAGGTAATA 20288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20195 AACTTAACACAATTACAAAAAGACAACTTGAAGCATCAA.....GTTGA 20238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20389 TAATTACAATACTGCTGTAAATAATGCAAATGGTGTTATTAATGCAACGA 20438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20289 CGTTAAATACTGCCATGGGTGCATTACGTACAAGTATCCAAAATGATAAT 20338
20706 CTGATAAAGAAAGAACAAAAGCAAGCGGTAATTATGTCAATGCTGATCAA 20755
                                                                                                                                                                                                                                                                                  20571
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                                                                                                                                          192
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                                         209 luAsp.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71 eLeuLysGluThrValArgGlnIleArgGlnIleLysGluGlnGlyLysT 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55 AsnLeuSerAspIleAspAsnPheAsnValLysProAspLysCysAlaIl 71
                                                                                                                                        rHisThrPheAsnCysArgMetLeuMetLysThrProHisAspIleLeuG 209
                                                                                                                                                                                                                                                                                ATGACTTAAACCAAAAACAA.....AAAGATGCATTAAAAACACAAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCAAATCAAGTCAATACAACAAAAGCAGCGTTAAATGGTGCACAAAACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            erLeuGlyProLeuLeuGlnAlaLeuAspGlyPheLeuPheValVal 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AspValGlnLysAla......AspValSerSerThrGlyGln.. 105
                                                                                                                                                                                      AACAATGCACAACGTGTATCTGATGCAAATAACGTTCAACACACTGCAAC 20664
                                                                                                                                                                                                                               AsnGly......ValSerTrpThrAsnGluProGlnArgGlnLysSe 192
                                                                                                                                                                                                                                                                                                                         isGluGluAspArgLysAspPheLeuLysAsnLeuProLysSerThrVal
                                                                                                                                                                                                                                                                                                                                                                        AGCTCAAGCTAAAACAAATGCGACGAACACA....ATTAACAACGCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AsnArgGluAlaAsnIleValPheValSerGluAsnValThrGlnTyrLe 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACAATCCAAATATGGATGCTAATGCGATTAATGGC.....ATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACGACGAAAACAAGTCAAAATTATCTTGATGCATCTGACAGCAACAAAAA 20388
                                                                                            TGAATTGAACAGTGCGATGACAGCACTTAAAGCA
                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 31096 base pairs TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (301) 610-5790
TELEFAX: (301) 309-8439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 216.00
0.299
48.069
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                                         .....IleAsnAlaSerPro 215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PB248P1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to: 31096
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                                                                                            GCTATTG
                                                                                                                                                                                                                                                                                                                              178
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                                                                                                                                                                                                                                                                                  20614
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528608

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1106

528373

524	\laSerSerGlyAsnThrGlyAsnHisSerPheSerSerSerSerLeuSe	508
21409	ACAACAGTAGCTGGTGTAAATCAAGAAACT	8
507	.sGlnPheSerProValAlaGlyValHisSerProMet	491
21379	AAAAAGATGCGTTAACGCGTAGCATTGATGGTGCA	21338
491	GlnGlnAsnIleMetIleSerProArgAsnArgGlySerProL	474
21337	AACTTAACATCAATTAAC	21314
474	TyrGlyLeuAsnMetSerSerProProHisGlySerProGlyLeuAl	458
ï		æ
57	uThrProGlyProGlyMetGlnSerProSerSerTyrGlnAsnAsn	441
441 21286	AlaArgTyrGlyGlySerSerAsnIleAlaS ::: ::: ::: TTAAATGGTGCGCGAAACTTAGCT.	424 21247
424 21246	euGlnMetProSerSerArgAlaTyrGlyLeuAlaAspProSerTh ::: ::: CGCAAGTAACATCACAA	408 21221
	 	7
07	tAlaGlyCysAsnSerSerValGlyGlyMetSerMetSerProAsnGln	
391 21173	OASnProAsnProValGlyGlnGlyIleArgProProM	37 4 21136
374 21135	AsnAspArgHisGlyPheValSerThrHisPheLeuGlnArgGluGlnAs ::: ::: ::: ::: AATGAAGCAACTAAAAGCAGGTCAAAACTACACTGACGCAAGTCCAAA	358 21086
357 21085	alThralaGlnThrLysSerLysLeuPheArgAsnProValThr 	341 21036
341 21035	LTyrArgPheSerLeuAlaAspGlyT ::: ::: :::::::::::::::::::::::::::::	324
1 2	AspóllyGlnSerTrpSerGlnLysArgHisTyrClnGluAlaTyrLe ::::: ::: ::::	5 5
0 0	STYTHEOLIASPITETTEATHATGYSTTECTHATGTHEFHESTELEHAAAGAGCATGCCAACAATACAATTGACGGCTTAGCACAATTGAAAGAGCATGCCAACAATACAATTGACGGCTTAGCACAATTG	<u> </u>
0 0	GCTAAAACAGCATTAAATGGTGATAACAACTTACGTGTAGCG	7
20871 291	CGACATTAACAGTCAATGACGTAAATAGTGCGGCATCACAAGTCAATG	20822 282
282	rPheIleThrArgHisAspLeuSerGlyLysVal	266
265 20821	rgArgIleThrThrGlyGluArgThr ::::: :::: :::AAAGTGACTAACGCTGAAAATATC	249 20780
20779		20779
249	${ t spLeuGlnSerCysMetIl}$	232
0	CGTATGATTCA	20756
232	erametargeriargiyrerunnaeterntysenearaneasereiner	0.17

α ν ·	 euAspA	22088 797
TleProSerSerSerGlnG 780	LysMetSerGlnCysThrSerSerThrIleProSerSerSerGlnG ::: ::	765 22039 780
alGluGlyValAspAsn 764 ::: ::: AACGGTATTCAMAACTT 22038	AspAlaLeuSerLysGluLeuGlnProGlnValGluGlyValAspAsn ::: ::: AACGGTATTCAMAAC	749 22022
uAspArgAspAspProSer 748	ysGluAsnAsnAlaLeuLeuArgTyrLeuLeuAspArgAspAs : ::: AAGCAAATACTGCATTA	732 22005
.GlnGluGlnLeuSerProLysLysL 732 :::::: TGAAAGAGCAATGCAAGCTGTTACAC 22004	PGlyAsnValValLys	718 21955
erIleThrSerCysGlyAs 718 :::::::: ::: TTTTAAATAAAACAGCTGG 21954	GlnAlaThrGlyLysAspThrSerSerIleThrSerCysGlyAs	704 21905
UValAlaLysIleThrala 703 : TGATGCTAAACGAACTGCT 21904	euLeuGlnAsnGlyAsnSerProAlaGluValAlaLysIleThrAla :: :: ::: CGTTACAAAGTCAAAATTATCAAGATGCTGATGATGCTAAACGAACTGCT	688 21855
IleLeuHisLysL 688 ATTCGTGATAAAGACACGA 21854	tHisGlySerLeuLeuGlnGluLysHisArgTleLeuHisLys.:	673 21805
erGlyGlyValSerSerThrSerAsnMe 673	SerGlyValSerSerThrSerGlyGlyVal::: :::::: GAAGGTGTTAATACAGTTAAA	657 21767
rvalServalThrSerPro 656 :::::::: ::: TACACAAGCAACAATGTT 21766	erProLeuAspSerSerCysLysGluSerSerValSerValThrSerPro:::::::::::::::::::::::::::::::::::	640 21717
HisSerSerLeuThrAsnS 640 ::: ACATTAACACACATTAATA 21716	nLeuLeuThrCysSerSerAspAspArgGlyHisSerSerLeuThrAsnS: :::::::::::: ::::::::::::: AGCTAAAGCAGCTGCGAAACAAACGTTAGGTACATTAACACACATTAATA	623 21667
xLysGlyHisLysLysLeuLeuGl 623 	GluAsnGlnArgGlyProLeuGluSerLysGlyHisLysLysLeuLeuG:::::	607 21623
uSerSerValGluGlyAla 606 -::::::::::::::::::::::::::::::::::::	rgAspHisLeuSerAspLysGluSerLysGluSerSerValGluGlyAla :::::	590 21579
MetCysGlnSerAsnSerA 590 ::: TTAACAAAAGCTAGTGGTC 21578	eTyrCysAspGlnAsnProValGluSerSerMetCysGlnSerAsnSer	573 21539
erLysSerProLeuGlyPh 573 :: AAGCA21538	ThrGlnProSerLysValSerAsnGlnAspSerLys :::::: CAGAGCCAAGTAAGAAATCAGCTTATGATCAAGCA	557 21503
nSerProAsnMetAsnIle 556	euSerSerProGlyProLysLeuAspAsn: ::::::	541 21474
ThrSerLeuLeuSerThrL 541 ::: GATGAGACAC 21473	rAlaLeuGlnAlaIleSerGluGlyValGlyThr :::::::::::: ::::: GCAATGCATAGTTTACAAAATGGTATCAATGAT	524 21434
21433	GCAAAAGCAACAGAATTAAATAAC	21410

50TZZ	GCATTAAAAGCACAAGTAACAAGTGCAGGACGTGT	22143
813 22144	rAsnAsnSerIleSerSerAsnGlySerHisLeuGlyThrLysG :::	828 22193
828 22194	InGlnValPheGlnGlyThrAsnSerLeuGlyLeuLysSerSerGlnSer::::::::::::::::::::::::::::::::::::	844 22243
845 22244	ValGlnSerIleArgProProTyrAsnArgAlaValSerLeuAspSerPr:::::::::::::::::::::::::::::::::::	861 22293
861 22294	AsnIle. ::::: ACGTTAA	873 22343
874 22344	SerAlaPheProMetLeuProLysGlnPro ::: ::: CACCAGCAGATGTTACAAATGCAGCAACGCAACTAAGTACGAATGCTAAGACG	883 22393
884 22394	etLeuGlyGlyAsnProArgMetMetAspSerGlnGluAsnTyrGly:: ::: 	99 244
900	SerSerMetGlyGlyProAsnArg TGCAATTGATGGTTTAACTTCTTTAAATGGTCCGCAAAAAGCAAAACTTA	907 22493
908 22494	ASGAACAAGTGGGTCAAGCGACGACGTTGCCAAATGTTCAAACTGTTCGT	911 22543
912 22544	ThrGlnThrProSerSerGlyAspTrpGlyLeuProAsnSer::: ::::::: ::: GATAATGCACAAACATTAAACACTGCAATGAAAGGTCTACGAGATAGCAT	925 22593
926 22594	LysAlaGlyArgMetGluProMetAsnSerA ::: TGCGAATGAAGCAACGATTAAAAGCAGGTCAAAACTACACAG	936 22634
936 22635	euProArgPro	952 22666
953 22667	.euArgSerAsnSerIlePr :::::::::: AGTGCAGTCAC	969 22677
969 22678	tLeuGlnMetArgP	986 22696
986 22697	lyAlaAsnProTyrGlyGlnAlaAla ::::: CAACTAGTCCATCAATGAATGCGCAA	1002 22729
1003 22730	nLeuGlySerTrpProAspGlyMetLeuSerMetGluGl 	1019 22770
1019 22771	nAsnArgProLeuLeuArg	1031 22811
1032 22812	AsnSerLeuAspAspLeuValGlyProProSer ::: ::: ATGCGAAGCAACATTTGAACGGCTTAAGTGACTTAACTGACGCTCAAAAA	1042 22861
1043 22862	ASDLeuGluGly	1046 22911

23721	ACTGTTATCAATCA	23708
1314	GlnGlnPheProTyrGlnProAsnTyrGlyMetGlyGlnGlnProAspPr	1298
1297 23707	roSerMetAspGlyLeuLeuAlaGlyProThrMetProGlnAlaProPro ::: :: !! ::::: CAACTGCACAAGGTATTATTGATCAAACTACAAGTCCAACTTTAGATCCG	1281 23658
1281 23657	nGlnThrGlnalaPheSerProProProAsnValThrAlaSerP : : : : : : : : : : : : : : :	1266 23608
1266 23607	GlnGlnGlnGlnGlnGl ::: :: :: AGATAATGCGACAACAAAACAAAACCAAAA	1261 23558
1260 23557	InGlnGlnGlnGlnGlnGlnGln	1253
1253 23507	nGlnArgValAlaMetMetMetGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnG	1236 23458
1236 23457	GlnMetValAlaGlnArgSerArgGluLeuLeuSerHisHisPheArgGl::::::	1220 23408
1219 23407	laAlaValMetArgProMetMetGlnProGlnGlnGlyPheLeuAsnAla ::::::::::::::::::::::::::::::::::	1203 23358
1203 23357	aLeuGluLeuLysMetGluAsnProThrAlaGlyGlyA	1190 23308
1190 23307	LeuGlnGlyGlnGlnPheLeuAsnGlnSerArgGlnAl :::::: :::: ATTGAAGGTGCGACAACAGTTGCAGGTGTAAATCAAGTGTCTACAACGGC	1178 23258
1177 23257	rgProArgThrAsnThrProLysGlnLeuArgMetGlnLeuGlnGlnArg :: :::	1161 23208
1161 23207	nGlyAsnPheProLeuGlnGlyMetHisProArgAlaAsnIleMetA ::::	1145 23158
1145 23157	GlyGlnSerProSerPheAsnSerMetMetAsnGlnMetAsnGlnGl ::	1130 23108
1129 23107	InThrTyrProAlaGlnGlyProProMetGlnGlyGlyPheHisLeuGln :::AAAGCACAAGGTCCAAATACTTCAAAAGAC	1113 23078
1113 23077	nGlyGlnGluAlaAlaValMetMetAspGlnLysAlaGlyLeuTyrGlyG ::: :::::::::::::: ACAAATGCAGTGACGCAAGCTGAACAAATTTTAAAT	1096 23042
1096 23041	GluLeuValAsnGlnGlyGlnAlaLeuGluProLysGlnAspAlaPheGl:::	1080 22994
1079 22993	snThrAspAlaThrGlyLeuGluGluIleAspArgAlaLeuGlyIlePro	1063 22956
1063 22955	.GlnSerAspGluArgAlaLeuLeuAspGlnLeuHisThrLeuLeuSerA :::::: ::: ::::: ACAAGCACAAAATAATGCGGATGCATTAAATACAGCTATGACGA	1047 22912

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Seq_documentation_block:
Sequence 12208, Application US/09335032
GENERAL INFORMATION:
APPLICANT: Velculescu, Victor
APPLICANT: Velculescu, Victor
APPLICANT: Velculescu, Bert
APPLICANT: Vogelstein, Bert
APPLICANT: Vogelstein, Bert
ITILE OF INVENTION: Characterization of the Yeast
TITLE OF INVENTION: Transcriptome
FILE REFERENCE: 01107.78572
CURRENT FILING DATE: 1999-06-16
PRIOR FILING DATE: 1999-06-16
PRIOR FILING DATE: 1997-01-23
PRIOR FILING DATE: 1997-01-23
PRIOR FILING DATE: 1998-01-22
NUMBER OF SEQ ID NOS: 12219
SOFTWARE: FasteEQ for Windows Version 4.0
SEQ ID NO 12208
LENGTH: 574860
Type: DNA
ORGANISM: Saccharomyces cerevisiae
US-09-335-032-12208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_block:
US-09-041-994-2 x US-09-335-032-12208/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:US-09-335-032-12208
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Percent Similarity:
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                                                                                                                                                                                                                                                                                                                       426855 ACTCAAGGATATTCCTTAGACGACTCAGGGATCCCCCGCTTGACTTCGAC 426806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1314 OAlaPheGlyArgValSerSerProProAsnAlaMetMetSerSerArgM 1331
||| |||:::||||||:::
||||||:::|
23722 AGCTGCTGGACAAGTAAGCACTAAAAAATGCATTAAATGGTAAT.... 23767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23768 ......GAAAACCTAGAGGCAGCGAAACAA 23791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23942 AAACAA 23947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23892 ATCAAATTAAGCAAAATGCGCAAAACTTAAATACAGCGATGGGTAACTTG 23941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23842 ACAAACAGTTACTGATCAAATTAATGGCGCGCATACTGTTGATGAAGCAA 23891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23792 CAAGCGTCACAATCATTAGGTTCATTAGATAACTTAAATAATGCGCAAAA 23841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1377 snProAlaValTyrSerMetValHisMetAsnGlySerSerGlyHisMet 1393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1364 nSerSerPheSerGlnGln...GlnPheAlaHis..........GlnGlyA 1377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1348 TyrGlnSerSerGluMetLysGlyTrpProSerGlyAsnLeuAlaArgAs 1364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1331 etGlyProSerGlnAsnProMetMetGlnHisProGlnAlaAlaSerIle 1347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1394 GlyGln 1395
                                                                                                                                    57
74 GluThrValArgGlnIleArgGlnIleLysGluGlnGlyLysThrIleSe 90
                                                                                                                                                                                                                                                        40 nGluSerLysTyrIleGluGluLeuAlaGluLeuIleSerAlaAsnLeuS 57
                                                                                                                                                                                                                                                                                                                                                                     24 ThrProGlyGlnGlyLeuThrCysSerGlyGluLysArgArgArgGluGl 40
                                                                                                                          erAspIleAspAsnPheAsnValLysProAspLysCysAlaIleLeuLys 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                216.00
0.324
45.498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length: 1466
Gaps: 66
Percent Identity: 19.236
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122 426603	AspGlyPheLeuPheValValAsnArgGluAlaAsnIleVa	135 426554
135 426553	PheValSerGlussnValThrGlnTyrLeuGlnTyrLysG	149 426504
149 426503	InGluAspLeuValAsnThrSerValTyrAsnTleLeuHisGluGluAsp::::::::::::::::::::::::::::::::::::	165 426454
166 426453	alse ATAG	182 426413
182 426412	rTrpThrAsnGluProGlnArgGlnLysSerHisThrPheAsnCysArgM	199 426394
199 426393	etLeuMetLysThrProHisAspIleLeuGluAspIleAsnAlaSerPro :::: :::::aGTCTTAAGAAACCACATAGCGTAGACTTTACTTCATCAACATCG	215 426349
216 426348	GluMetArgGlnArgTyrGluThrMetGlnCysPheAlaLeuSerGlnPr::: :::	232 426299
232 426298	OATGAlaMetMetGluGluGlyGluAspLeuGlnSerCysMetIleCysV ::: :::	249 426256
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262 426210	SerasnProGluSerPheIleThrargHisAspLeuSerGlyLysValVa :::	278 426161
278 426160	lasnIleAspThrAsnSerLeuArgSerSerMetArgProGlyPheGluA :::::: :::::::::::::::::::::::::::::	295 426114
295 426113	spIleIleArgArgCysIleGlnArgPhePheSerLeuAsnAspGlyGln:: AACAG	311 426109
312 426108	SerTrpSerGlnLysArgHisTyrGlnGluAlaTyrLeuAsnGlyHisAl	328 426077
328 426076	aGluThrProValTyrArgPheSerLeuAlaAspGlyThrIleValThrA:: :::	345 426037
345 426036	laGlnThrLysSerLysLeuPheArgAsnProValThrAsnAspArgHis ::::::::	361 425989
362	GlyPheValSerThrHisPheLeuGlnArgGluGlnAsnGlyTyrArgPr ::: :::	378

	1	rSerProSerGlyValSerSerS	62
	662		678
4	25183	eriniserglyelyedserserniserasmechiselyserheuben	N ~
	679 25133	GlnGluLysHisArgIleLeuHisLysLeuLeuGlnAsnGlyAsnSerPr::: ;;	695 425084
4	695 25083	oAlaGluValAlaLySIle	707 425034
_	707	1yLys	708
			708
4.	24983	ATATACGAAATTCCAATTTATACGAACTGATTACAGAAGTGCTGTATAA	424934
4	709	GATAATCAGCAAAAAGGAAGAAGCTCTTTCAGTTACTTGGGAAGGAC	719 424887
4	719 24886	lyAsnValValLysGlnGluGlnLeuSerProLysLysGluAsnAsn ::: ::: :::	735 424837
4	736 24836	AlaLeuLeuArgTyrLeuLeuAspArgAspAspProSerAspAlaLe::::	751 424787
4	751 24786	USerLysGluLeuGlnProGlnValGluGlyValAspAsnLysMetSerG	768 424749
	768 24748	<pre>InCysThrSerSerThrIleProSerSerSerGlnGluLysAspProLys I</pre>	784 424708
4	785 24707	IleLysThrGluThrSerGluGluGlySerGlyAspLeuAspAsnLeuAs	801 424675
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4	818 24643	erSerAsnGlySerHisLeuGly	825 424594
4	826 24593	ThrLysGlnGlnValPheGlnGlyThrAsnSerLeuGlyLeuLysSerSe GGTCCTAGAGACAGCCATAATTCGATTGGTTCAATTGCATTCCCCAGTAA	842 424544
4	842	rGlnSerValGlnSerIleArgProProTyrAsnArgAlaValSerLeuA :::::: ::: TTCGGGTGTTCAAAATATTCGCCGCTCTGTGTCCTTAT	859 424506
	859 2 4 505	SpSerProvalser	863 424456
4	864 24455	ValGlySerSerProProVa	870 424406

1175	$\verb nileMetArgProArgThrAsnThrProLysGlnLeuArgMetGlnLeuG $	1158
1158 423827	MetAsnGlnGlyAsnPheProLeuGlnGlyMetHisProArgAlaAs ::::::::: ::: CAAAGAGAAGATGGTTCGGAATATGTTAATATATCTAGCCTGGAAAA	1142 423873
1141 423874	<pre>LsLeuGlnGlyGlnSerProSerPheAsnSerMetMetAsnGln :: ::: :: :::: </pre>	1127 423914
1127 423915	GlyGlnThrTyrProAlaGlnGlyProProMetGlnGlyGlyPheH ::::: AATAGGATCCAGCACTCCA	1112 423943
1111 423944	GlnGlyGlnGluAlaAlaValMetMetAspGlnLySAlaGlyLeuTyr	1096 423993
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1079 424023	rAsnThrAspAlaThrGlyLeuGluGluIleAspArgAlaLeuGlyIleP ::::: GACCTTGATTCACAGCTAGGTATTT	1062 424047
1062 424048	GlyGlnSerAspGluArgAlaLeuLeuAspGlnLeuHisThrLeuLeuSe ::::: TCTGATTCTGAT	1046 424059
1045 424060	euLeuArgAsnSerLeuAspAspLeuValGlyProProSerAsnLeuGlu:::: ::: ::: :::::::::::::::::	1029 424103
1029 424104	pGlyMetLeuSerMetGluGlnValSerHisGlyThrGlnAsnArgProL 	1012 424134
424135		424135
1012	${\tt AsnProTyrGlyGlnAlaAlaAlaSerAsnGlnLeuGlySerTrpProAs}$	996
995 424135	InGlnMetLeuGlnMetArgProGlyGluIleProMetGlyMetGlyAla::::: ATGATCCATTGAAGAACAGAGGAACAGAAATACCT	979 424169
979 424170	OLeuArgSerAsnSerIleProGlyAlaArgProValLeuGlnGlnGlnG ::::: 	962 424182
424183		424183
962	As n Thr Ser Leu Pro Arg Pro Ala Leu Gly Gly Ser I le Pro Thr Leu Proposition (Leu Proposition Leu Proposition (Leu Proposi	946
945 424183	rgMetGluProMetAsnSerAsnSerMetGlyArgProGlyGlyAspTyr::::::	929 424217
929 424218	rGlnThrProSerSerGlyAspTrpGlyLeuProAsnSerLysAlaGlyA	912 424255
912 424256	GluAsnTyrGlySerSerMetGlyGlyProAsnArgAsnValThrValTh::: ::: ::: ::: :::::::::::::::::	896 424305
895 424306	euProLysGlnProMetLeuGlyGlyAsnProArgMetMetAspSerGln :: ::: TTCCCACAGAACCTACGAGATATAATTACCAAAATTTGGACTCTAGTAAG	879 424355
879 424356	LysasnIleSerAlaPheProMetL ::::::	870 424405

c	; SEC ID NO		CURRE	; TITLE ; FILE		; APPLI							seq_docume ; Sequence ; GENERAL : APPLICA	seq_name:	423333	1315	423383	1299	1282 423433	423483	1270	423533	1269	1254 423583	423633	1238	423668	1221	1204 423703	1188 423726	1175 423776	423826
TH: 3690	pt_FL_gen	OF SEQ ID NOS: 271	NT APPLICATION NUMBER: US/09/654,935A	OF INVENTION: REFERENCE: 793	OF INVENTION: N	Wang, zh	APPLICANT: Wehrman, Tom		APPLICANT: Many, otan-not APPLICANT: Ren, Feivan	Asundi, Vin	Zhou	Liu, Che	documentation_block: Sequence 142, Application US/09654935A GENERAL INFORMATION: APPLICANT: Tang, Y. Tom	e: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:US-09-654-935A-142	GCCTTTATGCCTTCTGCAGTGAATACTGGAC	Alaphe	GATTCAGTACTCAGACGACACATTCCACATCTGCTCTATTCATGAATCCT 423334	<pre>lnPheProTyrGlnProAssnTyrGlyMetGlyGlnGlnProAspPro ::; </pre>	rmetAspGlyLeuLeuAlaGlyProThrMetProGlnAlaProProGlnG 1299	TCCATCAAATTCTCACAGGCGCCTTCCACTCAGATCTCACCTAGGACTTC 423)AlaPheSerProProProAsnValThrAlaSerProSe 1282	CTTTAAAATTTGCATCAAGTTCCCCGATCTCGGAGGGATTCAGGAAATCG 423484		nGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln					aValMetArgProMetMetGlnProGlnGlnGlyPheLeuAsnAlaGlnM 1221 ::::: ::: ::: AGTCTTGAAAAAGGTAAAAAAGGTATTACAAG 423669	ArgGlnAlaLeuGluLeuLySMetGluAsnProThrAlaGlyGlyAlaAl 1204 :::::: :: AAGGAAGCAATCGAATTATCCAA 423704	InGlnargLeuGlnGlyGlnGlnPheLeuAsnGlnSer 1187	TATGGTCTCACCCAATGCACTACCACCTGTCGACTATGTCATGAAGTCTA 423777

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alignment_scores:
    Quality:
    Ratio:
Percent Similarity:
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; LOCATION: (55)..(3690)
US-09-654-935A-142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_block:
US-09-041-994-2 x US-09-654-935A-142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: US-09-654-935A-142 from: 1 to: 3690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                718 CATGGATCTGGGAATCTGTGCAATAGCAGTGATGGCTTTGGGAACCCCCAG 767
                                                                                                                                                                                                                                                               618 CAGCTGCAGTTTGGACCAAACGTCCAACAAAGAGGATGCTGGGTCGCTGT 667
                                                                                                                                                                                                                                                                                          555 nIleThrGlnProSerLysValSerAsnGlnAspSerLysSerProLeu. 571
                                                                                                                                                                                                                                                                                                                                               571 CCGCATTTAGCAACTCCTGGCTATTCCACTCCCACAAGT...AACATGAG
                                                                                                                                                                                                                                                                                                                                                                             539 SerThrLeuSerSerProGlyProLysLeuAspAsnSerProAsnMetAs 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              421 TATAATTGTAGAAACAACCTGGCCTTCCCAGCCCACCCCCAAGATGTGGA 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          494 SerHisGlnPheSerProValAlaGlyValHisSerProMet......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        467 oHisGlySerProGly.....LeuAlaProAsnGlnGlnAsnI 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  274 CGCCACTGGAATGAGGGCCATGCCACCATTCTTCACAGGACTTAGACCC 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         453 SerTyrGlnAsnAsnAsnTyrGly.....LeuAsnMetSerSerProPr 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         224 ACCACCTCATCTCCAGGCATGCTGTGAAAGGTGATCCTCAGTCTCCCGGT 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 437 erAsnIleAlaSerLeuThrProGlyProGly...MetGlnSerProSer 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            177 GGAAAGTTAAAAGTTCTGGCTCA...TCACATGCAAGGATAAAATCCAGAG 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          404 SerProAsnGlnGlyLeuGlnMetProSerSerArgAlaTyrGlyLeuAl 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  522 erLeuSerAlaLeuGlnAlaIleSerGluGlyValGlyThrSerLeuLeu 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      127 TCCTCTTCCGAGGTCATCGCTATTCCCACTGCTCAGAGTGCGGGACAGCG 176
768 GCACAGCGTGATCAATGTTTTTGTTGGAAGAGCTCAGAAAAACCAAGGGG 817
                                                                                                                                                                                                                                                                                                                                                                                                                                           AGCCCTGGGAATACAAATCCTCAGGTAATGGAAGGGCATCCCCCTGAAG 570
                                                                                                                                                                       ATTCTGAGGACCACGATGGCTACTGTGCATCTGTGCACACTGACTCTGGA
                                                                                                                                                                                                 .....AlaSerSerGlyAsnThrGlyAsnHisSerPheSerSerSerS 522
                                                                                                                            ProValGluSerSerMetCysGlnSerAsn............ 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       215.50
0.396
43.625
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Gaps: 61
Percent Identity: 20.529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               507
                                                                                                                                                                                                                                                                                                                                                    617
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802 1633	<pre>eLysThrGluThrSerGluGluGlySerGlyAspLeuAspAsnLeuAspA :::::::::: :::::::::: TTCTTCTAGTACTTCTACTGAAGGAAGTGGCACTATGAAGAAGCTGGATC</pre>	785 1584
5 5	TATCTTCAGTATCCATTTCCTCATCGTCCACTTCTCT	4-
л	sThrserserThrTleDroserserserGlnGlnIvsAspDroIvsTl	_1
768 1545	erLysGluLeuGlnProGlnValGluGlyValAspAsnLysMetSerGln::	752 1505
752 1504	uLeuArgTyrLeuLeuAspArgAspAspProSerAspAlaLeuS ::: :::: :::::::::::::::	737 1455
1454	TTTCTCCATCCAGTGGGTATTCCAGCCAGTCGAATACACCCACAGCACT.	1405
737	aLe	735
734 1404	ValLysGlnGluGlnLeuSerProLysLysLysGluAsn ::::!! ::: GTGGTTCAGTCAAACCAAAGATCATGTCACCAGAGAGTCACACAGAGTC	722 1355
1354	CGCCATGTCCAAGAAGGGTCCAGAGCCACAATGCCCCAAGTGCCCG	1305
721	- al	720
1304	CCGCAGGGGGCTGTTCAACCAGCAGTGGGGTGCCCACTGGGAACGGGCC	1255
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1254	:::	1243
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1242	attgactacacggcatgcaggaa	1212
687	lnGluLysHisArgIleLeuHisL	678
1211	::: ::::::::::::::::::::::::::	1162
677	erSerThrSerAsnMetHisGlySerLeu	668
1161		1112
667		659
659 1111	SerSerValSerValThrSerProSerGlyV	649 1062
1061	GCAGCTCGCCCTCCCAGAGCCCCTGCAGTGACTTGGAAGAGCC	1012
648	nSerProLeuAspSerSerCysLysGlu	639
638 1011	AGAGCCTGATCGCCACACTCCAGCACTCGCTGCAGCTTGAGCCTTCCCAGGC	634 962
961	CCAGTGCAACGGGCAGGTGCTCAACG	912
633		621
911		868
621	yAlaGluAsnGlnArqGlyProLeuGluSerLysGlyHisLysLysLe	605
604 867	erArgAspHisLeuSerAspLysGluSerLysGluSerSerValGlu ::: ::::: ::::: ::::: :: ::::: ::::: ACCGGTCCAATTACCAGGATAAATCCCTATCAAGAAACATCTCTTTGAAG	589 818

1074	LeuLeuSerAsnThrAspAlaThrGlyLeuGluGluIleAspAr	850
2394	GGGGAGGCAGAGGCTCGG	
1057	oSerAsnLeuGluGlyGlnSerAspGluArgAlaLeuLeuAspGlnLeu	041
2368	TGGAGCTC	
	G nAsnArgDroLenLenArgAsnSerLenAsnAsnLenWalG vDroD	250
1024	ProAspGlyMetLeuSerMetGluGlnValSerHisGlyThr	011 284
2283	AAATGAAATGGAGAGTGAAAGCCAGCCTGCCTCTGTGACAAGCTCGC	234
1010	LeuGlySerTrp	007
2233	agtaccacttaaagccatctgctttcctgaaatcccgaaatag	184
1006		900
1006 2183	nProTyrGlyGlnAlaAlaAlaSerAsnGln	995 134
μ	::: :::	084
994	${\tt lnMetLeuGlnMetArgProGlyGluIleProMetGlyMetGly}$	978
978 2083	rAsnSerIleProGlyAlaArgProValLeuGlnGlnG ::: ATAACCACGGAAG	961 064
961 2063	AlaLeuGlyGlySerIleProThrLe	945 041
944 2040	AsnSerAsnSerMetGlyArgProGlyGlyAsp	928 015
928 2014	ThrProSerSerGlyAspTrpGlyLeuProAsnSerLysAlag 	911 968
911 1967	luAsnTyrGlySerSerMetGlyGlyProAsnArgAsnValThrVa 	895 921
894 1920	:LeuGlyGlyAsnProArgMetMetAspSer	879 871
879 1870	rProProValLysasnIleSerAlaPheProMetL 	862 827
862 1826	nSerIleArgProProTyrAsnArgAlaValSerLeuAspSerProVa 	846 777
845 1776	GlyLeuLysSerSer.GlnSerVal + -	835 727
835 1726	LeuGlyThrLysGlnGlnValPheGlnGlyThrAs ::: ::: TGTCCTGCAGACAGGTCTCCTTCCTTCCTCCCC	819 677
1676	ccerecererccccceecrccrccrccrccrccr	634

1279	1263 3134	1247 3084	3081	3053	3003	1182 2971 1198	1167 2921	1164 2871	1147 2833	1139 2783	1131 2733	1114 2683	1107 2633	2583	1096 2533 1102	1087 2483	1074 2433	2395
laSerProSerMetAsp	nGlnGlnGlnThrGlnAlaPheSerProProProAsnValThrA 1: :::::: ::: ::::::: ::: ::::::::	GlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnG	CHOCK LIBERT & STRUCTURE A STATE CHARGE CHARGE CHARGE CHARGE THE CHARGE			nPheLeuAsnGlnSerArgGlnAlaLeuGluLeuLysMetGluAsn 1:	ProLysGlnLeuArgMetGlnLeuGlnGlnArgLeuGlnGlglnGl 1:	» ·	nPheProLeuGlnGlyMetHisProArgAlaAsnIleMetArgProArgT 1:		GlnSerProSerPheAsnSerMet			GGAGGCAAAAGAGAGTTCTGCAGCCCAAGCTGGCTCTCATG	TGTGCCCAGCCCACGACGGAGAGGAGGAGGCTCTGT:	AlaLeuGluProLysGlnAspAlaPhe	gAlaLeuGlyIleProGluLeuValAsnGlnGlyGln	::: ::::: ::: :::
287	183	.263)133	3083	080	052	197	1182 2970	.166 !920	.164 2870	1147 2832	1138 2782	1130 2732	1114 2682	632	1102 2582 1106	1095 2532	1086 2482	432

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eq_name: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:US-09-335-032-12218
<pre>sq_documentation_block: sq_documentation_block: Sequence 12218, Application US/09335032 GENERAL INFORMATION: APPLICANT: Velculescu, Victor APPLICANT: Vogelstein, Bert APPLICANT: Kinzler, Kenneth TITLE OF INVENTION: Characterization of the Yeast TITLE OF INVENTION: Transcriptome FILE REFERENCE: 01107.78572</pre>
CURRENT APPLICATION NUMBER: US/09/335,032 CURRENT FILING DATE: 1999-06-16 PRIOR APPLICATION NUMBER: US 60/035,917 PRIOR FILING DATE: 1997-01-23 PRIOR APPLICATION NUMBER: US 09/012,031 PRIOR APPLICATION NUMBER: US 09/012,031 PRIOR FILING DATE: 1998-01-22 NUMBER OF SEQ ID NOS: 12219 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 12218
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2 1	lGlyProProSerAsnLeuGluGlyGlnSerAspGl 105	. 0
CTAGES	230	40
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Sequence 703, Application US/09813206
GENERAL INFORMATION:
APPLICANT: Gearing, David P.
APPLICANT: Holtzman, Douglas A.
APPLICANT: Holtzman, Douglas A.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM A
TITLE OF INVENTION: HUMAN CORONARY ARTERY SMOOTH MUSCLE I
FILE REFERENCE: 1600.1023-002
                                                                                                                                                                                                                                                                                                 seq_name: /cgn2_6/ptodata/2/pna/US09_NEW_COMB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ...SerGlyHisMetGlyGlnMetAsnMetAsnProMetProMetSerGl
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US/09/813,206
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US-09-813-206-703
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PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 09/338,425
PRIOR FILING DATE: 1999-06-22
NUMBER OF SEQ ID NOS: 934
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                                                                                                                                                                           TCTCTTCCAGGGGAAGCCTTNCGGCACCAGGGGATCCCCTTCACGACCCA
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                                         .....AlaSerHisGlnPheSerPro.....Val.AlaGlyV 503
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Ratio:
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523 3341	uSerAlaLeuGlnAlaIleSerGluGlyValGlyThrSerLeuLeuS 5	39 292
539 3 2 91	erThrLeuSerSerPro	48 242
549 3241	AspAsnSerProAsnMetAsnIleThrGlnProSerLysValSerAsnG1 5	65 222
565 3221	nAspSerLysSerProLeuGlyPheTyrCysAspGlnAsnProValGluS 5 :::::: :::	82 190
582 3189	erSerMetCysGlnSerAsnSerArgAspHisLeuSerAspLysGluSer 5 ::: ::::: GCCTTCTTTGCCAGCCAGNACCCAGGAGGGCCAGGGGGTCCAAGCATTTT 3	98
599 3139	LysGluSerSerValGluGlyAlaGluAsnGlnAr 6 ::::::::::::::::::::::::::::::::::::	090
610 3089	gGlyProLeuGluSerLysGlyHisLysLysLeu	040
622 3039	GGCTCCCAGGAGCCACCCAAACATTACCAATGGGGCCAGGGGGTCCATTC 2	28 990
629 2989	GGGTCCCGGCAAGGGCCAAGGGGGACCAAGCATCGCCTTTTAAGCACCAA	40 940
640 2939	rProLeuAspSerSerCysLysGluSerSerValSerValThrSerProS 6 : :: :::::::::: :::: :::::: ::::::	57 890
657 2889	erGlyValSerSerSerThrSerGly.GlyValSerSerThrSerAs 6 :: ::: :::	72 840
672 2839	nMetHisGlySerLeuLeuGlnGluLysHisArgIleLeuHisLysLeuL 6 ::::	89 817
689 2816	euGlnAsnGlyAsnSerProAlaGluValAlaLysIleThrAlaGlnAla 7 :::::: :::	05 785
706 2784	ThrGlyLysAspThrSerSerIleThrSerCysGlyAspGlyAspValVa 7 ::: : ::: :::	22 752
722 2751	llysGlnGluGlnLeuSerProLysLysLysGluAsnAsnAlaLeuLeuA 7	39 712
739 2711	rgTyrLeuLeuAspArgAspAspProSerAspAlaLeuSer 7 ::: ::::::::::::::::::::::::::::::::	52 662
753	LysGluLeuGlnProGlnValGluGlyValAspAsnLysMetSerGlnCy 7	69

1968	.CCATCAGGACCAGGAAATGCCAGGGCT	1994
1057	roSerAsnLeuGluGlyGl	1040
1995	GACCAGGGGGCCAGTTTTG	2015
1040	lnAsnArgProLeuLeuArgAsnSerLeuAspAspLeuValGlyPr	1024
2016	ccc:	2060
1023	/MetLeuSerMetGluGlnValSe	1007
2061	:::	2075
1007	oMetGlyMetGlyAlaAsnProTyrGlyGlnAlaAlaAlaSerAsnGlnL	990
2076	ATCACCACCAAGCCT	2090
990	ValLeuGlnGlnGlnGlnMetLeuGlnMetArgProGlyGluIlePr	974
2091	TTCTCCAGCAGCCACCTTTTAGGTCCCAGGGAATCCCC	2128
973	erIleProThrLeuProLeuArgSerAsnSerIleProGlyAlaArgPro	957
2129	TCCGGGAAAAAACCTTCGGCTTTCCAAGCCTTGGCCG	2169
957	aLeuc	940
940 2170	snSerLysAlaGly.ArgMetGluProMetAsnSerAsnSerMetGlyAr::	924 2201
2202	CTCC	2223
924	<pre>gAsnValThrValThrGlnThrProSerSerGlyAspTrpGlyLeuProA</pre>	907
2224	CAAGGGGTCCC	2235
907	- K	891
2236	CTTGTTCACCTCTCCTCCCCAAGCGGGACCAGCAGGGC	2273
890	LysGlnProMetLeuGlyGlyAsnProArg	875
874 2274	OValSerValGlySerSerProProValLysAsnIleSer :::	861 2323
2324	CCCTTGTTCACCAAGGTTTTGCCCTGCCTTCACCTGGAAGGAC	2373
861	— н	848
2374	TCTCGCCTCCTTGCTCCAGAGGGGCCAGGGCAGCCAAGGTTCTCCAAGG	2423
847	heGlnGlyThrAsnSerLeuGlyLeuLysSerSerGlnSerValGlnSer	831
831 2424	nAsnSerIleSerSerAsnGlySerHisLeuGlyThrLysGlnGlnValP :::::::: :::::::::::::::::::::::::::	814 2464
2465	CGTTGCCGGGAAGCAACCGTTGGCCCCTCGGGGACCCAGCAAGGACCAGG	2514
814		801
800 2515	ysileLysThrGluThrSerGluGluGlySerGlyAspLeuAspAsnLeu :::	784 2564
2565	CACCACGGTTCACCAGGCATTCC	2611
784		769
2612	GACCAAGCATCACCTTCTTGTCACCCTTTAGGCCCCTGGAAGACCAGCGTG	2661

	1299 1265
tAspGlyLeuLeuAlaGlyProThrMetProGlnAlaProProGln 1298	1283 1308
ProAsnValThrAlaSerProSerMe 1283	1275 1358
InGlnGlnGlnGlnThrGlnAlaPheSerProPro	1262 1408
GlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnG	1246 1458
euLeuSerHisHisPheArgGlnGlnArgValAlaMetMetMetGlnGln 1245 ::: ::: ACCAGGAGCACCATTGGCACCCTTTAGCAACCAGNGCTGTCCATCAGCAC 1459	1229 1508
LeuAsnAlaGlnMetValAlaGlnArgSerArgGluL 1229	1217 1558
GlyPhe	1215 1608
lyAlaAlaValMetArgProMetMet	1202 1658
aLeuGluLeuLysMetGlusnProThrAlaGlyG 1202	1190 1708
LeuGlnGlnArgLeuGlnGlyGlnGlnPheLeuAsnGlnSerArgGlnAl 1190 ::::::	1174 1758
laAsnIleMetArgProArgThrAsnThrProLysGlnLeuArgMetGln 1173 	1157 1790
nGlnMetAsnGlnGlnGlyAsnPheProLeuGlnGlyMetHisProArgA 1157 : ::	1140 1819
GlyGlyPheHisLeuGlnGlyGlnSerProSerPheAsnSerMetMetAs 1140	112 4 1869
ysAlaGlyLeuTyrGlyGlnThrTyrProAlaGlnGlyProProMetGln 1123	1107 1872
OLYSG1nAspAlaPheG1nG1yG1nG1uAlaAlaValMetMetAspG1nL 1107 ::::::	
ArgAlaLeuGlyIleProGluLeuValAsnGlnGlyGlnAlaLeuGluPr 1090	1074 1941
euHisThrLeuLeuSerAsnThrAspAlaThrGlyLeuGluGluIleAsp 1073	1057 1967

<u> </u>	UNKNOWN A: A: 60/127, ER: 60/127, ATION: 1ana 1ana BER: 30,930	COUNTRY: USA ZIP: 08512 COMPUTER READABLE FORM: COMPUTER READABLE FORM: COMPUTER: IN Compatible OPERATING SYSTEM: DOS SOFTWARE: N/A CURRENT APPLICATION DATA: APPLICATION UMBER: US/09/543,679A FILING DATE: 13-Apr-2000	seq_documentation_block: Sequence 3003, Application US/09543679A GENERAL INFORMATION: APPLICANT: NYCE, Jonathan W. TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLECTID COMPOSITIONS, KIT & METHOD FOR TREATMEN OF AIRWAY DISORDERS ASSOCIATED WITH BRONCHOCONSTRICTION, LUNG INFLAMMATION, NUMBER OF SEQUENCES: 3111 CORRESPONDENCE ADDRESS: ADDRESSE: POIGNESIS PHARMACEUTICALS, INC. STREET: 7 Clarke Drive CITY: Cranbury	1399 nProMetProMetSerGlyMetProMetGlyProAsp 1411	1371 lnPheAlaHisGlnGlyAsnProAlaValTyrSerMetVal 1384	1345 AlaSerIleTyrGlnSerSerGluMetLysGl 1355	erAr	1312 ProaspProAlaPheGlyArgValSerSerProProAsnAlaMetMetSe 1328 ::: ::: 1221GCTCCAGGGGGCGACCTCCTCCTCACCAGGCAGGGCCACGGG 1181

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;; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 3003:
US-09-543-679A-3003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_block:
US-09-041-994-2 x US-09-543-679A-3003/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality: 210.00
Ratio: 0.382
Percent Similarity: 43.273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to reverse of: US-09-543-679A-3003 from: 1 to: 35459
                                                                                                        5812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5999
5762 GCAAGCAGCAGAAACCCCGGGGAGGCAGCCAVVGVCCVCCCCACGGCAVG 5713
                                                                                                                                                                                                           5938 GCCAGGACGCCCGAGGAGGAGGACGGCGCGACAGAGACAG...... 5898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6049 CCCACCACACCCCAACCCAGCGGCCCCACACCACCAGACAGGCCCAG 6000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6090 CGC...CCACAGAGACACCCAACAGCCCCAC.....AGGCCACAGAAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6108 ......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6145 GGGGGGGGGGGGGCGCGCACCAGCACAGGGAGGAA......6109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6195 CAGGGCAAGAGCCCAGAAGCGCCCACAAGGAGCCAGCACCGGCCCAGAA 6146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6295 TCTCCATGGCCATCAGGTAGCTCACGTCGGCCAGCACCGCCTCCAGGTCC 6246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6245 GCCATCTTGGCGGCGGCGCGCAGCCCAGCAGCCACGAGGCGAAGAAGGA 6196
                                                                                                                                   564 snGlnAspSerLysSerProLeuGlyPheTyrCysAsp...... 576 ::||| :::|||::: |||
                                                                                                                                                                                                                                                            547 sLeuAspAsnSerProAsnMetAsnIleThrGlnProSerLysValSerA 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          514 lyAsnHisSerPheSerSerSerSerLeuSerAlaLeuGlnAlaIleSer 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        481 etIleSerProArgAsnArgGlySer.ProLysIleAlaSerHisGlnPh 497 :::||| :::||||||||||||
                                                                                                                                                                                                                                                                                                                                                                        531 GluGlyValGlyThrSerLeuLeuSerThrLeuSerSerProGlyProLy 547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   497 eSerProValAlaGlyValHisSerProMetAlaSerSerGlyAsnThrG 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   465 rProProHisGlySerPro...GlyLeuAlaProAsnGlnGlnAsnIleM 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       449 GlnSerProSerSerTyrGlnAsnAsnAsnTyrGlyLeuAsnMetSerSe 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            432 rgTyrGlyGlySerSerAsnIleAlaSerLeuThrProGlyProGlyMet 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               415 gAlaTyrGlyLeuAlaAspProSerThrThrGlyGlnMetSerGlyAlaA 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           394 sAsnSer.SerValGlyGlyMetSerMetSerProAsn...... 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   379 AsnProAsnProValGlyGlnGlyIleArgPro...ProMetAlaGlyCy 394 :::||| ||| ||| ||| |||
                                                                                                  GCAACCAGCCGGCCGGCGGGGGAGCACCG......5970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .....GlnAsnProValGluSerSerMetCysGlnSerAsnSerAr 590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .........GCCCCAAGACCCAGCACA 6091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length: 1271
Gaps: 62
Percent Identity: 19.512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6050
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851	SerSerGinSerValGinSerIleArgProP	841
840 4886	LysGlnGlnValPheGlnGlyThrAsnSerLeuGlyLeuLys :::	827 4935
4936	erasprietyrasiasibetiteetserasib.lysera.sieddyfir 	4976
ت و د	SerGlyAspLeuAspAsnLeuAspAlaIleLeuGlyAspLeuThr CGGGGGGACCCA	793 4993 810
793 4994	GlnGluLysAspProLysIleLysThrGluThrSerGluGluGl 	779 5043
778 5044	alAspAsnLysMetSerGlnCysThrSerSerThrIleProSerSerSer ::::::::::::::::::::::::::::::	762 5086
762 5087	AGACCGCCGCAAGGGCACCGGCAACCAGCCAGACCCGAGCAGAAGGCC	757 5136
756 5137	LeuAspArgAspAspProSerAspAlaLeuSerLysGluLeuGln	742 5186
741 5187	luGlnLeuSerProLysLysLysGluAsnAsnAlaLeuLeuArgTyrLeu ::: ::: ::: AGCGGCGGCGGAAGAGGAAGGAGGGCGGGCGGAACAGCACAAG	725 5230
725 5231	sAspThrSerSerIleThrSerCysGlyAspGlyAspValValLysGlnG :::: :: ::	708 5265
708 5266	GlyAsnSerProAlaGluValAlaLysIleThrAlaGlnAlaThrGlyLy::: :::: :::: :::: :::: ::::	692 5315
691 5316	ysHisArgIleLeuHisLysLeuLeuGlnAsn	681 5365
681 5366	1SerSerThrSerAsnMetH1sG1ySerLeuLeuG1nG1uL::: :::: :: ::	667 5415
667 5416	ValSerValThrSerProSerGlyValSerSerSerThrSerGlyGlyVa ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: :: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: :: :: ::: ::: ::: ::: ::: ::: ::: ::: :: ::: ::	651 5465
650 5466	erCysLysGluSerSer :::::::: :::::::: aggCagAAgagCcCAggGAACAGCAGGAGGCGGGGACCCCCGGCGGAGAA	645 5515
645 5516	ThrAsnSerProLeuAspSerS	638 5565
637 5566	LeuLeuThrCysSerSerAspAspArgGlyHisSerSerLeu	62 4 5615
623 5616	luAsnGlnArgGlyProLeuGluSerLysGlyHi8LysLysLeuLeuGln ::: ::: :::: :::: ccCGCCGCGACCCAGGAGGGGACGACGCGACGGACGGAC	607 5662
5663	gAspHisLeuSerAspLysGluSerLysGluSerSerValGluGlyAlaG ::: ::: ::: ::: ::: ::: ::: ::: ::: :	590 5712

1087	1070 4128	1058 4178	1043 4228	1029 4278	1025 4328	1009 4378	992 4428	980 4475	963 4507	946 4524	933 4571	916 4615	900 4662	898 4712	881 4750	868 4800	851 4835	4885
laLeuGluProLysGlnAspAlaPheGlnGlyGlnGluAlaAlaValMet	uGluIleAspArgAlaLeuGlyIleProGluLeuValAsnGlnGlyGlnA:	H1sThrLeuLeuSerAsnThrAspAlaThrGlyLeu	snLeuGluGlyGlnSerAspGluArgAlaLeuLeuAspGlnLeu ::	LeuLeuArgAsnSerLeuAspAspLeuValGlyProProSerA	GlnAsnArgProGlnAsnArgProGlnAsnArgProGlnAsnArgProGlnAsnArgProGlnAsnArgProGlnAsnArgProGlnAsnArgProGlnAsnArgProGlnAsnArgPro	SerTrpProAspGlyMetLeuSerMetGluGlnValSerHisGlyThr	yMetGlyAlaAsnProTyrGlyGlnAlaAlaAlaSerAsnGlnLeuGly.	GlnMetLeuGlnMetArgProGlyGluIleProMetGl	euArgSerAsnSerIleProGlyAlaArgProValLeuGlnGlnGlnGln ::::::: GAGAGAGGCAGAAGAGCCCAGGGAACAGCAG	nThrSerLeuProArgProAlaLeuGlyGlySerIleProThrLeuProL: ::		rSerGlyAspTrpGlyLeuProAsnSerLysAlaGlyArgMetGluProM ::::	SerSerMetGlyGlyProAsnArgAsnValThrValThrGlnThrProSe:::::: ::: ::: ::: ::: ::: ::: ::: ::: :::	YIG1Y	SGlnProMetLeuGlyGlyAsnProArgMetMetAspSerGlnGluAsnT	ProProValLysAsnIleSerAlaPheProMetLeuProLy	roTyrAsnArgAlaValSerLeuAspSerProValSerValGlySerSer	CCCCGCACCCCAAGACGCCAGGCGCAGGCAGCAGGAAACCCAGCCCC
1103	1087 4097	1070 4129	1057 4179	1043 4229	1028 4279	1024 4329	1008 4379	992 4429	979 · 4476	963 4508	946 4525	933 4572	916 4616	899 4663	898 4713	881 4751	867 4801	4836
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												-						
3259 GVVA				3459 AGGG	3509 GGAG	3559 CCCA			3685 AVGG	3735 ACCC	3785 CCCC		3885 CCCC					4096 CAGC

1290 ProThrMetProGlnAlaProProGlnGlnPheProTyrGlnProAsnTy 1306 ::: :::::: 3259 GVVAVAAAACCCCAAGACVGGAAAGGAAACCA 3228	
1280SerProSerMetAsp	
ωμ	
1249 GlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnG	
1247Glngln 1248	
GTCAGGAGAGGGAAGACGGGCGGAACACAGGGACAG	
1246	
1237 lnargValalametMetMetGlnGlnGln	
1220 nmetValAlaGlnArgSerArgGluLeuLeuSerHisHisPheArgGlnG 1237	
1208ProMetMetGlnProGlnGlnGlyPheLeuAsnAlaGl 1220	
G .	
1187 rArgGlnAlaLeuGluLeuL 1194 :	
1171 rgMetGlnLeuGlnGlnArg.LeuGlnGlyGlnGlnPheLeuAsnGlnSe 1187	
1162ProArgThrAsnThrProLysGlnLeuA 1171	
1151 GlnGlyMetHisProArgAlaAsnIleMetArg 1161	
1134 erPheAsnSerMetMetAsnGlnMetAsnGlnGlnGlyAsnPheProLeu 1150 ::	
1117 aGlnGlyProProMetGlnGlyGlyPheHisLeuGlnGlyGlnSerProS 1134 ::: ::: 3998 .CGCGGACCCCAGGAAACGGGCGGG	
1104 MetAspGlnLysAlaGlyLeuTyrGlyGlnThrTyrProAl 1117 ::::::	
4096 CAGCCAGACCCCGAGCAGAAGGCCAGGGGGGGGGGGACCACC	

```
APPLICANT: Volculescu, Victor
APPLICANT: Vogelstein, Bert
APPLICANT: Vogelstein, Bert
APPLICANT: Kinzler, Kenneth
TITLE OF INVENTION: Characterization of the Yeast
TITLE OF INVENTION: Transcriptome
FILE REFERENCE: 01107.78572
CURRENT APPLICATION NUMBER: US/09/335,032
CURRENT FILING DATE: 1999-06-16
PRIOR APPLICATION NUMBER: US 60/035,917
PRIOR FILING DATE: 1997-01-23
PRIOR FILING DATE: 1998-01-22
NUMBER OF SEQ ID NOS: 12219
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12214
LENGTH: 666448
TYPE: DNA
                                                                                                                                                                                                                            alignment_scores:
Quality:
Ratio:
Percent Similarity:
                                                                                                                                           alignment_block:
US-09-041-994-2 x US-09-335-032-12214/rev
                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Saccharomyces cerevisiae US-09-335-032-12214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_documentation_block:
; Sequence 12214, Application US/09335032
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:US-09-335-032-12214
                                                                                                   Align seg 1/1 to reverse of: US-09-335-032-12214
338119 CCAAATCCAGAAGATGATATTACATATAAGAGTTCTAATAATAGCAATTC 338070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1366 SerPheSerGlnGlnPheAlaHisGlnGlyAsnProAlaValTyrSe 1382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1399 snPro 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2939 CGCGCCCAGGCGAACGGGCAGAACACACACAGGGCAAAGGACCAGCG 2890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1382 rMetValHismetAsnGlySerSerGlyHismetGlyGlnmetAsnmetA 1399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3127 VVCVVCCCVCVGAAATCVGCAGVAVCAGCVCCCAGCAGAAACACACAGGG 3078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1306 rGlyMetGlyGlnGlnProAspProAlaPheGlyArgValSerSerProP 1323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2889 GACCC 2885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2989 ANGGCAACAGACCGGAGAACGGCGGGGAGAAACCCCACGAGGAACCCGCAG 2940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3227 GCAVVVGCVCAGGCAGCCVCVCVGGGAAGAVGCVGCVVCVVCCVCCCCC 3178
                                          446 ProGlyMetGlnSerProSerSerTyrGlnAsnAsnAsnTyrGlyLeuAs 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tGlnHisProGlnAlaAlaSerIleTyrGlnSerSerGluMetLysGlyT 1356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .....MetMetSerSerArgMetGlyProSerGlnAsnProMetMe 1339
                                                                                                                                                                                                                            207.50
0.549
43.852
                                                                                                                                                                                                                            Length: 862
Gaps: 33
Percent Identity: 19.142
                                                                                                   from: 1
                                                                                                   to: 666448
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776	lGluGlyValAspAsnLysMetSerGlnCysThrSerSerThrIleProS	759
337449		337486
759	AspArgAspAspProSerAspAlaLeuSerLysGluLeuGlnProGlnVa	743
742 337487	InLeuSerProLysLysGluAsnAsnAlaLeuLeuArgTyrLeuLeu ::: :::::::: :::: CATCTGCACAAGAACAAGAGGAGGAGGACTGCT	726 337518
726 337519	PThrSerSerIleThrSerCysGlyAspGlyAsnValValLysGlnGluG	709 337562
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662 337713	CysLysCluSerSerValSerValThrSerProSerGlyValSerSerSe	646 337759
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337331 824	TACAGTTGTTGAAeuGlyThrAsnSerLeuGlyLeuLys	337319 840
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12216, INFORMAT IT: Velc IT: Vog IT: Kin INVENT INVENT ERENCE: APPLICAT FILING PLICATI	/cgn2_6/ptodata/2	Ginginginginginginthyginala TTCCAACAACAACAGCAACAGCTGCC	lnGlnGlnGlnGlnGlnG ::: CAACCTGTTAACCCAC		gGluLeuLeuSerHisHis	GlnProGlnGlnGlyPhe	ysMetGluAsnProThrAl	:	gLeuGlnGlyGlnGlnPh	ArgProArgThrAsnThr ::: CATTCTGAAGACTCTCAA	lnGlnGlyAsnPheProL -:: -::	OI ATACCAGTTACCAAAGAA	AlaGlnGlyProProMet :::TATGGTCAACCTCAA	laAlaValmetMetAspG ::::: GTGGCTCATTCATGCCAT	nGlnGlyGlnAlaLeuGluProLySGlnAs ::::: ::: TCACGCCCAACCTCAACAA	ThrGlyLeuGluGluIle ::::: ::: GCTAATTTGACTAGTGCT	luArgAlaLeuLeuAspG ;; ;;; AATATAATTTCCAACAAG	C
block: Application US/09335032 ION: ION: Ulescu, Victor elstein, Bert zler, Kenneth ION: Characterization of the ION: Transcriptome 01107.78572 TION NUMBER: US/09/335,032 DATE: 1999-06-16 ON NUMBER: US 60/035,917 TE: 1997-01-23	/pna/US09_NEW_COMB.	GlnThrGlnAla 1270 ::: CAAGCTGCTGCC 336269	Ginginginginginginginginginginginginging		PheArgGlnGlnArgVa	InProGinGinGlyPheLeuAsnAlaGinMetValAlaGinArgSer : : :	aGlyGlyAlaAlaValMe		${f gLeuGlnGlyGlnGlnPheLeuAsnGlnSerArgGlnAlaLeuGluLeuLucucucucucucucucucucucucucucucucucu$	ArgProArgThrAsnThrProLysGlnLeuArgMetGlnLeuGlnGlnAr::: ::	<pre>lnglnglyAsnPheProLeuGlnglyMetHisProArgAlaAsnIleMet :::</pre>	OSerPheAsnSerMetMetAsnGlnMetAsnG 	.aGlnGlyProProMetGlnGlyGlyPheHisLeuGlnGlyGlnSerPr 	laalaValMetMetAspGlnLysAlaGlyLeuTyrGlyGlnThrTyrPro :::::	aLeuGluProLysGlnAspAlaPhe	ThrGlyLeuGluGluIleAspArgAlaLeuGlyIleProGluLeuValAs :::::: ::: GCTAATTTGACTAGTGCTGCCGCTGCTGCTGCCGCTTCTCCAGCTACAGC	luargalaLeuLeuAspGlnLeuHisThrLeuLeuSerAsnThrAspAla ::: ::	GCTCAAACTAGTGGTAATGCTAACC
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246 I 514782 I	MetileCysValalaArgArgTleThrThrGlyGluArgThrPheProSe 262	
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laG1 607	AspHisLeuSerAspLysGluSerLysGluSerSerValGluGlyAlaG ::: ::: :::::::::::::::::::::::::::	591 515844
Arg 590 ACA 515843	yrCysAspGlnAsnProValGluSerSerMetCysGlnSerAsnSerArg:::::::::::::::::::::::::::::::::::	574 515797
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سو		Ō
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640 515975	euLeuThrCysSerSerAspAspArgGlyHisSerSerLeuThrAsnSer 	62 4 515926
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                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: US-08-899-336-2
                                                                                                                                                                                         alignment_block:
                                                                                                                                                                                                                                                                                alignment_scores:
                                                                                                                                                                                                                          Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2,
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78 eGlnGlyGlnGluAla.....
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COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
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                                                                                                                                                                                                                                                              Quality:
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seq_documentation_block:
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/cgn2_6/ptodata/1/ina/6A_COMB.seq:US-09-022-696-1
/cgn2_6/ptodata/1/ina/6A_COMB.seq:US-08-978-773-1
                                                                     Align seg 1/1 to: US-08-899-336-2 from: 1 to:
                                                                                                         US-09-041-994-2_COPY_1018_1179 x US-08-899-336-2
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                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (703) 413-2220 INFORMATION FOR SEQ ID NO: :
                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 25
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 23-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 800 PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
907 CCACAACAATCGGGGCAAGGGCAACAGCTGGGACAAGGGCCAACAACCAGG 956
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
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                                 62 ProGluLeuValAsnGlnGlyGlnAlaLeuGluProLysGlnAspAlaPh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 1755 SOI
CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: 23-JU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Application US/08899336 5955649
                                                                                                                                                                                                                                                                                                                                          nucleic acid
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Y: U.S.A.
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KURODA, HISAO
ITO, KAZUTOSHI
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                                                                                                                                                                                                                                                                                                                                                           2296 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HIROTA,
                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                    (703) 413-3000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UMBER: US/08/899,336
23-JUL-1997
                                                                                                                                                                                                                                                                                       DNA (genomic)
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MAKOTO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENE EXPRESSION REGULATORY DNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JP HEI 8-193433
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                                                                                                                                                             Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2589-0061-0
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AlaValMetMetAspGlnLysAlaGlyL 93

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alignment_scores:
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 Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No. 6175000
                                                                                                                                                                                                                              TELEFAX: (619)546-9392
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/
FILING DATE: 13-MAY-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Reiter, Stephen E.
REGISTRATION NUMBER: 31,19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1207
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                                                                                                                                   TOPOLOGY: u
                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Pretty, Schroeder, Bru
STREET: 444 South Flower Street,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           957
                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: CHARACTERIZATION OF A CHROMOSOME 11023
TITLE OF INVENTION: TRANSLOCATION BREAKPOINT ASSOCIATED WI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                               TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 94:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                        TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTTCTCCGCAGCAGCCAGGACAAGGGCCAACAGCTAGGACAAGGGCCAACAA 1206
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                                         Quality:
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Selleri, Licia
Parry, Pauline
                                                                                                                                                                                                                                                                  (619)546-9392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
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                                                                                                                                                       unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                   UMBER: US/08/061,376
13-MAY-1993
85.50
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Flower Street, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4
   Percent Identity: 21.788
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alignment_block:
US-09-041-994-2_COPY_1018_1179 x US-08-061-376-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No. 5633135
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1,
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                                                                                                                                                                                                                                                                                  APPLICANT: Croce, Carlo
APPLICANT: Canaani, Eli
TITLE OF INVENTION: Diagnostics, Therapeutics and Methods for
TITLE OF INVENTION: Detection and Treatment of Acute Leukemias
TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the
TITLE OF INVENTION: All-1 Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7242 CGAACATATGGGATCTAGTTCCAGAGATAGGAGACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7142 ACACAGATTCTACCCAATCAGCAAACTCCTCTCCAGATGAAGATACTGAA
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                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
Woodcock Washburn Kurtz Mackiewicz & No.
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No.
STREET: One Liberty Place - 46th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7052 CTGAACCCTCTTCAGTGTCGTTTTCTTCTAAAGAGGCCCCTC...... 7092
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                                                COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               104 oMetGlnGlyGlyPheHisLeuGlnGlyGln.....
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COMPUTER: IBM PS
OPERATING SYSTEM:
                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTCAAAACCTTGAAGCTATCTGGAATGAGCAACAGATCATCCATTATCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGACTTGGTGTCCAAGAGCTCCTCTTTAAAGGGAGAGAAGACCAAA....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                laLeuLeuAspGlnLeuHisThrLeuLeuSerAsnThrAspAlaThrGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .....CACCTCCATTTGAGAGGGCAAAGGAATGATCGAGACCAAC 7141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .....GlyGlnAlaL 71
                                                                                                           19103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .....SerProSerPheAsnSerMetMetAsnGlnMetAsnGln 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Application US/08320559
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                                                                                                                                  USA
                         IBM PS/2
                                                DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
PC-DOS
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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: US-08-320-559-1 from: 1 to: 14255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-041-994-2_COPY_1018_1179 x US-08-320-559-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                       6751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (215) 568-3439 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                        6778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6705 AGACTTGGTGTCCAAGAGCTCCTCTTTAAAGGGAGAGAAGACCAAA.... 6750
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/062,443
FILING DATE: 14 MAY 1993
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US/07/971,094
                                                                                                                                                                                                                                         6828 TCATAACACAACATCTAGAGAACTGAATGTTAGTAAAATCGGCTCCTTTG 6877
104 oMetGlnGlyGlyPheHisLeuGlnGlyGln.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: TJ
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/805,093
FILING DATE: 11-DEC-91
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/888,830
FILING DATE: 27-MAY-92
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CURRENT APPLICATION DATA:
                                                                                               88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18 pAspLeuValGlyProProSerAsnLeuGluGlyGlnSerAspGluArgA 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35 laLeuLeuAspGlnLeuHisThrLeuLeuSerAsnThrAspAlaThrGly 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 SerHis.....GlyThrGlnAsnArgProLeuLeuArgAsnSerLeuAs 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 33,229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US, FILING DATE: 30-OCT-92
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                                                                                                                                                                                                                                                                                                                                                                                     LeuGluGluIleAspArgAlaLeuGlyIleProGluLeuValAsnGln.. 67
                                                                                            AspGlnLysAlaGlyLeuTyrGlyGlnThrTyrProAlaGlnGlyProPr 104
                                                                                                                                         CTGAACCCTCTTCAGTGTCGTTTTCTTCTAAAGAGGCCCCTC...... 6918
                                                                                                                                                                                         euGluProLysGlnAspAlaPheGlnGlyGlnGluAlaAlaValMetMet 87
                                                                                                                                                                                                                                                                                                                                        TCTGCACATAATGTGGCTTACCCTGGAATTCCTAAACTGGCCCCACAGGT 6827
                                                                                                                                                                                                                                                                                        nucleic acid
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0.983
48.603
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Percent Identity: 21.788
                                                                                                                                                                                                                                                                                                                                                                                                                                     .GTGCTGAGTTCCAAGAGCTCAGAGGGA 6777
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alignment_scores:
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                                                                                                                                 US-08-327-392-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_documentation_block:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/08327392
Patent No. 5633136
                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7018 GTCAAAACCTTGAAGCTATCTGGAATGAGCAACAGATCATCATTATCAA 7061
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7068 CGAACATATGGGATCTAGTTCCAGAGATAGGAGACAG 7104
                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 07/888,830
FILING DATE: 27-MAY-92
PRIOR APPLICATION DATA:
APPLICATION UNBER: 07/805,093
FILING DATE: 11-DEC-91
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              128 GlnGlyAsnPheProLeuGlnGlyMetHisProArgAlaAsnIleMetAr 144
                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/971,094
FILING DATE: 30-OCT-92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5633136ris
STREET: One Alberty Place - 46th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: ALL-1 Polynucleotides and Monoclonal TITLE OF INVENTION: Antibodies for Leukemia Detection and TITLE OF INVENTION: Treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          144 gProArgThrAsnThrProLysGlnLeuArgMetGln 156
                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Croce, Carlo APPLICANT: Canaani, Eli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJ
                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
                                                                                                                                                                                                                                       LENGTH:
                                                                                                                                                                                                                                                                                                                           TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: DeLuca, Mark
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .....SerProSerPheAsnSerMetMetAsnGlnMetAsnGln 127
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                                           Quality:
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                                                                                                                                                                                                                                                                                                       (215) 568-3439
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                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                              (215)
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85.50
0.983
48.603
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Gaps:
Percent Identity:
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                                           Length:
  21.788
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seq_name: /cgn2_6/ptodata/1/ina/5A_COMB.seq:US-08-306-691B-55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 55, Application US/08306691B Patent No. 5734039
                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: ANTISENSE
TITLE OF INVENTION: OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES
NUMBER OF SEQUENCES: 55
                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            144 gProArgThrAsnThrProLysGlnLeuArgMetGln 156
                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Calabretta, Bruno
APPLICANT: Skorski, Tomasz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35 laLeuLeuAspGlnLeuHisThrLeuLeuSerAsnThrAspAlaThrGly 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18
                      COMPUTER: IBM PS/
OPERATING SYSTEM:
                                                                                                                                    COUNTRY: UZIP: 19102
                                                                                                                                                                                                                                        STREET:
                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pAspLeuValGlyProProSerAsnLeuGluGlyGlnSerAspGluArgA 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AspGlnLysAlaGlyLeuTyrGlyGlnThrTyrProAlaGlnGlyProPr 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTGAACCCTCTTCAGTGTCGTTTTCTTCTAAAGAGGCCCTC..... 6918
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LeuGluGluIleAspArgAlaLeuGlyIleProGluLeuValAsnGln.. 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SerHis.....GlyThrGlnAsnArgProLeuLeuArgAsnSerLeuAs 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .....SerProSerPheAsnSerMetMetAsnGlnMetAsnGln 127
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T: Two Penn Center, Suite 1800
Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .....CACCTCCATTTGAGAGGGCAAAGGAATGATCGAGACCAAC 6967
                                                                                                                                                          Pennsylvania : U.S.A.
                                              IBM PS/2
WordPerfect 5.1
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                                                                             720 Kb
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alignment_scores:
Quality:
Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-041-994-2_COPY_1018_1179 x US-08-306-6918-55
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TELEFAX: (215) 568-54
TELEX: NO. 5734039e
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/(
FILING DATE: September 1
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                        6828 TCATAACACAACATCTAGAGAACTGAATGTTAGTAAAATCGGCTCCTTTG 6877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6655 AGTCACTTGGATGGATCTTCATCTTCAGAAATGAAGCAGTCCAGTGCTTC
7018 GTCAAAACCTTGAAGCTATCTGGAATGAGCAACAGATCATCCATTATCAA
                                                                                    6968 ACACAGATTCTACCCAATCAGCAAACTCCTCTCCAGATGAAGATACTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: MONACO, DAN161 A.
REGISTION NUMBER: 30,480
REFERENCE/DOKET NUMBER: 83:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION: NAME: Monaco, Daniel A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52 LeuGluGluIleAspArgAlaLeuGlyIleProGluLeuValAsnGln.. 67
                                                                                                                                                                                                                                                                                                                                                                                             71 euGluProLysGlnAspAlaPheGlnGlyGlnGluAlaAlaValMetMet 87
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                                      GlnGlyAsnPheProLeuGlnGlyMetHisProArgAlaAsnIleMetAr 144
                                                                                                                                                                                                                                                                                                      AspGlnLysAlaGlyLeuTyrGlyGlnThrTyrProAlaGlnGlyProPr 104
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                                                                                                                  .....SerProSerPheAsnSerMetMetAsnGlnMetAsnGln
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(215) 568-5549
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September 15, 1994
NN: 514
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Percent Identity: 21.788
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Gaps:
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; ANTI-SENSE: US-08-545-860D-1
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                                                                                                                      TELEFAX: (215) 568-3439 (INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7068 CGAACATATGGGATCTAGTTCCAGAGATAGGAGACAG 7104
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APPLICATION NUMBER: PCT/US94/04496
FILING DATE: 22-APR-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
FILING DATE: 27-MAY-1
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                       FILING DATE: 11-DEC-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
FILING DATE: 14-MAY-
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/327,392 FILING DATE: 19-OCT-1994 PRIOR APPLICATION DATA:
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                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: (215) 568-3100
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TITLE OF INVENTION: for Detection and Treatment of Acute Leukemias
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                                                        TYPE: nucleic acid
STRANDEDNESS: singl
                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 07/971,094 FILING DATE: 30-OCT-1992
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                                       TOPOLOGY:
                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                  REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
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FILING DATE: 09-DEC-1992
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27-MAY-1992
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                                                                                                       APPLICANT: Canaani, Eli
TITLE OF INVENTION: Diagnostics, Therapeutics and Methods
TITLE OF INVENTION: for Detection and Treatment of Acute |
TITLE OF INVENTION: Resulting from Chromosome Abnormaliti
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                                                                                               CORRESPONDENCE ADDRESS:
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                      STREET:
                                          ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewitz & ADDRESSEE: Norris
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Philadelphia
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                    One Liberty Place, 46th floor
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48.603
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Pennsylvania

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; TOPOLOGY:
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PCT-US94-04496-1
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
                                                                                                                                  104 oMetGlnGlyGlyPheHisLeuGlnGlyGln.....
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LENGTH: 14255
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                               CTGAACCCTCTTCAGTGTCGTTTTCTTCTAAAGAGGCCCTC..... 6918
ACACAGATTCTACCCAATCAGCAAACTCCTCTCCAGATGAAGATACTGAA 7017
                                                                                                                                                                                                                               AspGlnLysAlaGlyLeuTyrGlyGlnThrTyrProAlaGlnGlyProPr 104
                                                                                                                                                                                                                                                                                                                           euGluProLysGlnAspAlaPheGlnGlyGlnGluAlaAlaValMetMet 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCTGCACATAATGTGGCTTACCCTGGAATTCCTAAACTGGCCCCACAGGT 6827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          laLeuLeuAspGlnLeuHisThrLeuLeuSerAsnThrAspAlaThrGly 51
                                                                                            .....CACCTCCATTTGAGAGGGCAAAGGAATGATCGAGACCAAC 696
                                              .....SerProSerPheAsnSerMetMetAsnGlnMetAsnGln 127
                                                                                                                                                                                                                                                                                                                                                                                                             .....GlyGlnAlaL 71
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48.603
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                                                                                                                                                                                   Percent Identity: 21.788
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alignment_block:
us-09-041-994-2_COPY_1018_1179 x us-08-227-536-1
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; LOCATION:
US-08-227-536-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: /cgn2_6/ptodata/1/ina/5A_COMB.seq:US-08-227-536-1
                                                                               Align seg 1/1 to: US-08-227-536-1 from: 1 to:
                                                                                                                                                                                        Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/08227536 Patent No. 5658784
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APPLICANT: Eckner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (617) 451-0313 INFORMATION FOR SEQ ID NO:
7329 GGCACTGTGTCTCAACAAGCCTTACAAAACCTTTTGCGGACTCTCAGGTC 7378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Ewen, Mark
APPLICANT: Livingston, David
APPLICANT: Livingston, David
TITLE OF INVENTION: NUCLEIC ACID, ENCODING TRANSCRIF
TITLE OF INVENTION: FACTOR P300 AND USES OF P300
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Weingarten, Schurgin, Gagnebin & Hayes
STREET: Ten Post Office Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7018 GTCAAAACCTTGAAGCTATCTGGAATGAGCAACAGATCATCCATTATCAA 7067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Williams Ph.D., Kathle
REGISTRATION NUMBER: 34,380
REFERENCE/DOCKET NUMBER: DEC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-2290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 9046 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    144 gProArgThrAsnThrProLysGlnLeuArgMetGln 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         128 GlnGlyAsnPheProLeuGlnGlyMetHisProArgAlaAsnIleMetAr 144
                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                    HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/227,536 FILING DATE: 14-APR-1994 CLASSIFICATION: 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: Ten I
                                     6 GlyThrGlnAsnArgProLeuLeuArgAsnSerLeuAspAspLeuValG1 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
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                                                                                                                                                                                                                                    Quality:
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1200..8441
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Percent Identity:
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                                                                                                                                                                                          23.529
                                                                                    9046
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7417 rccrrcicic 56 AspargalaLeucly1leProgluLeuvalAssnGlnGlyGlnAlaLeugl 72 7425	22 yProProSerAsnLeuGluGlyGlnSerAspGluArgAlaLeuLeuAspG 39 :
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alignment_block:
US-09-041-994-2_COPY_1018_1179 x PCT-US95-04682-1
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    Quality:
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ATTORNEY/AGENT INFORMATION:
NAME: Holliday C. Heine, Ph.D.
REGISTRATION NUMBER: 34,346
REFERENCE/DOCKET NUMBER: DFCI-301
TELECOMMUNICATION INFORMATION:
TELECHONE: (617) 542-2290
TELEFAX: (617) 451-0313
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: PCT-US95-04682-1 from: 1 to: 9046
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Percent Similarity:
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                                                                                         7609 AGGCGGGCGTTCAGAGGGCTGGCCTGCCCCAGCAGCAACCACCAGCAA
                                                                                                                                                                                  7559 TCAGCAGGGGGTCCACTCCAATCCAGCCATGCAGAACATGAATCCAATGC 7608
                                                                                                                                                                                                                                                                             7509 CCTGGCATGCCCCAGGGGCAGCCAGGGCTACAGCCCACCTACCATGCCAGG 7558
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7659 CTCCAGCCACCCATGGGAGGGATGAGCCCCCAGGCTCAGCAGATGAACAT '7708
                                      129 GlyAsnPheProLeuGlnGlyMetHisProArgAlaAsnIleMetArgPr 145
                                                                                                                                                                                                                                                                                                                           104
                                                                                                                                                                                                                             105 tGlnGlyGlyPheHisLeuGlnGlyGlnSerProSerPheAsnSerMet. 121
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                                                                                                                                                                                                                                                                                                                                                                                                             89 lnLysAlaGlyLeuTyrGlyGlnThrTyrProAlaGlnGlyPro..... 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72 uProLysGlnAspAlaPheGlnGlyGlnGluAlaAlaValMetMetAspG 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56 AspArgAlaLeuGlyIleProGluLeuValAsnGlnGlyGlnAlaLeuGl 72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22 yProProSerAsnLeuGluGlyGlnSerAspGluArgAlaLeuLeuAspG 39
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LOCATION:
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STRANDEDNESS: sing
TOPOLOGY: linear
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1200..8441
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Gaps: 7
Percent Identity: 23.529
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alignment_block:
us-09-041-994-2_COPY_1018_1179 x US-08-612-986-1
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                                                                                                                                                                                                                                                                                      alignment_scores:
                                                                                                                                                                                                                                                                                                                                                     US-08-612-986-1
                                                                                                                        Align seg 1/1 to: US-08-612-986-1 from: 1 to: 1071
                                                                                                                                                                                                                             Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 08/361,800
FILING DATE: 22 DEC 1994
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Paul L.
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: NEP-(TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECPHONE: (617) 227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (617) 227-594
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1071 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               145 oArgThrAsnThr...ProLysGlnLeuArg.....MetGlnLeuGlnG 159
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7709 GAACCACACACCATGCCTTCACAATTCCGAGACATCTTGAGACGACAGC 7758
                                        595 CCAGAGCATGGACAATTCCAAGGCAGTCCTGGTGGTGCCTATGGGACTGC 644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Elliot J. Androphy
APPLICANT: Dave E. Breiding
TITLE OF INVENTION: E2 BINDING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         159 lnArgLeuGln 162
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
  88
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                                                                              73 ProLysGlnAspAlaPheGlnGlyGlnGlu...AlaAlaValMetMetAs
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STATE: Massa
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CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: 11
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                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                        LOCATION: 1..1071
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pGlnLysAlaGlyLeuTyrGlyGlnThrTyrProAlaGlnGlyPro.... 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAATGATGCAA 7769
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                                                                                                                                                                                                                                                Quality:
Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                         84.00
1.647
41.803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       single
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                                                                                                                                                                                                                         Percent Identity:
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                                                                                                                                                                                                                     27.049
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seq_name: /cgn2_6/ptodata/1/ina/5A_COMB.seq:US-08-361-806A-1
; LOCATION:
US-08-361-806A-1
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                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/361,8068
FILING DATE: 22 DEC 1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Paul L
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: NEP-004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/08361806A Patent No. 5792833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                            TELEFAX: (617) 227-59 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           153 uArgMetGlnLeuGln 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   945 CCCTGTGCAGATGCAG 960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           895 CACCCCCAGGCTCTGCATCCAGCCCCTGGACTCCTTGCTTCCCCCCCAGCT 944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      137 HisProArgAlaAsnIleMetArgProArgThrAsnThrProLysGlnLe 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     845 ATGCTAACCAGCAGACTGGCTTCTCCGACTCATCCTCTGCGCCCCCATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             645 TCAGCCCCCACCTCACTATGGGCCCACACAGCCAGCTTATAGTCCTAGTC 694
                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Dave E. Breiding
TITLE OF INVENTION: E2 BINDING PROTEINS
                                                                    FEATURE:
                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 02109-1875
                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET:
                                          NAME/KEY:
                                                                                                                  TOPOLOGY:
                                                                                                                                                        TYPE: nucleic acid
                                                                                                                                                                               LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InmetAsnGlnGlnGlyAsnPhe.....ProLeuGlnGlyMet 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .....ProMetGlnGl 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Massachusetts
                                                                                                                                                                               1071 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60 State Street, suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Elliot J. Androphy
                1..1071
                                                                                                               linear
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                                                                                                                                  single
                                                                                                                                                                                                                                                  227-5941
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alignment_block:
US-09-041-994-2_COPY_1018_1179 x US-08-361-806A-1
; NAME/KEY:
; LOCATION:
PCT-US95-16806A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:PCT-US95-16806A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: US-08-361-806A-1 from: 1 to: 1071
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Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application PC/TUS9516806A GENERAL INFORMATION:
                                                                                                                                                                                                  FILING DATE: 22-DEC-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               845
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                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 22-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  945 CCCTGTGCAGATGCAG 960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          745 CCACAGCACCAGCCCTATGCTGCATGGCCACTTTCAGCCCACTCAGAC 794
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                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: E2 Binding Proteins NUMBER OF SEQUENCES: 21
                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88 pGlnLysAlaGlyLeuTyrGlyGlnThrTyrProAlaGlnGlyPro.... 103
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                                                                                                STRANDEDNESS:
TOPOLOGY: lin
                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: December
                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                             LENGTH:
                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        uArgMetGlnLeuGln 158
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                                                                                                                                        nucleic acid
                                                                                                                                                           1071 base pairs
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                  1..1071
                                                                                                    linear
                                                                                                                                                                                                                                                                                                     December
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1.647
41.803
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ber 22, 1995
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Gaps: 3
Percent Identity: 27.049
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seq_name: /cgn2_6/ptodata/1/ina/5A_COMB.seq:US-08-198-446B-8
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Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 8,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                             COUNTRY: USA
ZIP: 98101-2347
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                         SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          895
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APPLICANT: Grouding
TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Hartwell, Lela
APPLICANT: Weinert, Ted A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                153 uArgMetGlnLeuGln 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88 pGlnLysAlaGlyLeuTyrGlyGlnThrTyrProAlaGlnGlyPro.... 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73 ProLysGlnAspAlaPheGlnGlyGlnGlu...AlaAlaValMetMetAs
                  CLASSIFICATION:
                                       FILING DATE:
                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                               STREET:
                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CACCCCAGGCTCTGCATCCAGCCCCTGGACTCCTTGCTTCCCCCCAGCT
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                                                                                                                                                                                                                                                              Seattle
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                                                                                                                                                                                                                                                                                                                                                                               Groudine, Mark T
                                                                                                                                                                                                                                                                                                                                                                                                    Plon, Sharon E.
INFORMATION:
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                                   18-FEB-1994
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1.647
41.803
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                                                                                                                                                                                                                                                                                                                                           19
                                                                                              Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                          Leland H.
                                                        US/08/198,446B
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Percent Identity: 27.049
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6
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REFERENCE/DOCKET NUMBER: FH

FHCR17537

Sheiness, Diana K.

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alignment_block:
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INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1896 base pairs
LENGTH: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to reverse of: US-08-198-446B-8 from: 1 to: 1896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-041-994-2_COPY_1018_1179 x US-08-198-446B-8/rev
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linea
MOLECULE TYPE: CI
DESCRIPTION: h:
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1024 CTCGGTGCAGCAGTTCCATCACCACCCCTCTACTGCTCTCCATGGAGAAT 975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANTI-SENSE: NO ORIGINAL SOURCE: ORGANISM: Hom
                                                                                                                                                                                                       109
                                                                                                                125
                                                                                                                                                            701
                                                                                                                                                                                                                                                 751 GTCCGTACCAAGATACCCCAATGCTGTAGGATTCCCATCAAACAGTGGTC 702
                                                                                                                                                                                                                                                                                                                                          801
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                                                                                                                                                                                                                                                                                                                                                                             85 ValMetMetAspGlnLysAlaGlyLeuTyrGlyGlnThr.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69 ln...AlaLeuGluProLysGlnAspAlaPheGlnGlyGlnGluAlaAla 84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 ValSerHisGlyThrGlnAsnArgProLeuLeuArgAsnSerLeuAspAs 19
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                                                                   ATGAACACACAAACTATGCATCCTTCACAGCCTCAGGGAACTTATGCCTC 602
                                                                                                              MetAsnGlnGlnGlyAsnPheProLeuGln.....
                                                                                                                                                          AAGGACTAATGCACCAGCAGCCCATCCACCCCAGTGGCTCACTTAACCAA 652
                                                                                                                                                                                                  heHisLeuGlnGlyGlnSerProSerPheAsnSer...MetMetAsnGln 124
                                                                                                                                                                                                                                                                                    .....TyrPro...AlaGlnGlyProProMetGlnGlyGlyP 109
                                                                                                                                                                                                                                                                                                                                          ACAGGGATGAATCAAAATTTAGGCCTTACAAATAATACTCCAATGAATCA 752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 uGluGluIleAspArgAlaLeuGlyIleProGluLeuValAsnGlnGlyG
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                                                                                                                                                                                                                                                                                                                                                                                                                                AGTATTCTCGATATCCTTACAGTAACCTAAATCAGGGATTAGTTAACAAT 802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ......CAGACAGTCCCCTCTCCTACTATAAACAACTCAGGGC
......GlyMetHisProArgAlaAsnIleMetArgProArgThrAsnT 149
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Percent Identity: 25.926
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; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo
US-08-870-693-8
alignment_block:
US-09-041-994-2_COPY_1018_1179 x US-08-870-693-8/rev
                                                                                                              alignment_scores:
Quality:
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                                                                     Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 8, Application US/08870693 Patent No. 5866338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 08/198,446
FILING DATE: February 18, 1994
APPLICATION NUMBER: PCT/US93/04458
FILING DATE: May 12, 1993
APPLICATION NUMBER: US 07/884,426
FILING DATE: May 14, 1992
APPLICATION NUMBER: US 07/882,051
FILING DATE: May 12, 1992
APPLICATION NUMBER: US 07/882,051
FILING DATE: May 12, 1992
APPLICATION NUMBER: US 07/882,051
FILING DATE: May 12, 1992
ATTORNEY/AGENT INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              _documentation_block:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: cDNA to mRNA DESCRIPTION: human RAD9coi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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APPLICANT: Groudine, Mark T.
TITLE OF INVENTION: Cell Cycle Checkpoint Genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: 206-682-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Hartwell, Lelan APPLICANT: Weinert, Ted A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    551 CTCCTCCACAAGTCAGG 535
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CTTY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Sheiness, Diana K.
REGISTRATION NUMBER: 35,356
REFERENCE/DOCKET NUMBER: FH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TOPOLOGY: lin
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1420 Fifth Ave., Suite 2800
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UMBER: PCT/US93/04458
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0.988
44.444
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                                                   eaps: 8
Percent Identity: 25.926
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seq_name: /cgn2_6/ptodata/1/ina/5B_COMB.seq:US-08-525-742-5
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APPLICANT:
APPLICANT:
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                                                                                                     TITLE OF INVENTION: NEW POLYPEPTIDE, DAA ENCODING THE
TITLE OF INVENTION: POLYPEPTIDE, RECOMBINANT VECTOR BEARING THE DNA AND
TITLE OF INVENTION: RECOMBINANT VIRUS UTILIZING THE RECOMBINANT VECTOR AS WELL
TITLE OF INVENTION: AS USE THEREOF
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                                                                                        UMBER OF SEQUENCES:
                                                                                                                                                                                              APPLICANT:
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      1725 K Street,
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                                                                                                                                                                                                                                                   Ohsawa, Ikuroh
Funato, Hirono
                                                                                                                                                                                                                                                                                         Ohkawa, Setsuk
Saeki, Sakiko
                                                                                                                                                                               Iritani, Yoshikazu
Aoyama, Shigemi
Takahashi, Kiyoohito
                                                                                                                                                                                                                                                                                                                                      Saito, Shuji
                             NAUGHTON
                                            ARMSTRONG, WESTERMAN, HATTORI, MCLELAND
                                                                                                                                                                                                                                                                                                                   Setsuko
        Suite 1000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; LOCATION:
US-08-525-742-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: JP 05-
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP
FILING DATE: 31-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: MCLeland, Le-Nhung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 95
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-659-2930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: JP 0
FILING DATE: 31-MAR-1993
PRIOR APPLICATION DATA:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                            517
                                                                                                                                                                                                         467
                                        567 TGGTCATCCACAACACGGACCACGTCCGATGAATGCTCATCCAGGTCAAC 616
                                                                                                                                                                                                                                                                                         417 ACAATTAGTAACAACTGATGTAGCTAGCAATCAAGCTGCAGGTACTGAAC
                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                               54 luIleAsp...... 56
                                                                                                                                                                                                                                                                                                                           37 uAspGlnLeuHisThrLeuLeuSerAsnThrAspAlaThrGlyLeuGluG 54
                                                                                                                                                                                                                                                                                                                                                                                                          21 ValGlyProProSerAsnLeuGluGlyGlnSerAspGluArgAlaLeuLe
82 luAlaAlaValMetMetAspGlnLysAlaGlyLeuTyrGlyGlnThrTyr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
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                                                                                aLeuGluProLys......GlnAspAlaPheGlnGlyGlnG
                                                                                                                          CCAGCTCCTTCACCAATGGGTAGTCCTAAGTTATTAGGTCCAAACCAAGC 566
                                                                                                                                                                                                       .....ArgAlaLeuGlyIleProGluLeuValAsnGlnGlyGlnAl 70
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1.113
46.104
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Percent Identity:
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OM of: US-09-041-994-2_COPY_1018_1179 to: Pending_Patents_NA_Main:*

out_format :

/cgn2_6/ptodata/1/pna/US093_COMB.seq:US-09-338-425-2396 +

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530.38 530.38 530.38

2.6e-20 2.6e-20 .6e-20

2.6e-20

May 1,

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Sequence
/cgn2_6/ptodata/1/pna/US090
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Database sequences: 13168883
Database length: -1691701393
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search information block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Command line parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -MODEL-frame+_p2n.model -DEV-xlp
-Q-/cgn2_1/USPTO_spco1/US09041994/runat_30042001_165632_19506/app_query.fasta_1.1940
-Q-/cgn2_1/USPTO_spco1/US09041994/runat_30042001_165632_19506/app_query.fasta_1.1940
-DB-Pending_Patents_NA_Main -QEMTY-fastap -SUFFIX-P2n.rnpm
-GAPOP-12.000 -GAPEXT-4.000 -MINMATCH=0.100 -LOOPCL-0.000
-LOOPEXT-0.000 -GAPEXT-4.000 -MINMATCH=0.100 -LOOPCL-0.000
-YGAPEXT-0.500 -FGAPOP-6.000 -GAPEXT-7.000 -YGAPOP-10.000
-YGAPEXT-0.500 -DELOP-6.000 -DELEXT-7.000 -START-1
-MATRIX-blosum62 -TRANS-human40.cdi -LIST-45 -DOCALIGN=200
-THR_SCORE-pct -THR_MAX-100 -THR_MIN-0 -ALIGN-15 -MODE-LOCAL
-USER-US09041994_@CGN1_1_8354 -NCPU-6 -ICPU-3 -LONGLOG -NO_XLPXY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Results were produced by Copyright (c) 1993-2000
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00 Compugen Ltd.
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6835
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alignment_block:
US-09-041-994-2_COPY_1018_1179 x US-09-041-994-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: /cgn2_6/ptodata/1/pna/US090_COMB.seq:US-09-041-994-1
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/cgn2_6/ptodata/1/pna/US096C_COMB.seq:US-09-652-126-8996 + 312.5
/cgn2_6/ptodata/1/pna/US096C_COMB.seq:US-09-652-355-10385 + 312.5
/cgn2_6/ptodata/1/pna/US096C_COMB.seq:US-09-652-814-10217 + 312.5
                                                                                                                                                                                                                         Align seg 1/1 to:
                                                                                                                                                                                                                                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/09041994 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 617-742-4214 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Chen, J. D
APPLICANT: L1, Hu1
TITLE OF INVENTION: T
TITLE OF INVENTION: F
NUMBER OF SEQUENCES:
                                                                         3187
                                                                                                                                                    3137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: UM TELECOMMUNICATION INFORMATION: 617-227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Liepmann, W. Hugo
REGISTRATION NUMBER: 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: CDNA FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                    34
                                                                                      17 uAspAspLeuValGlyProProSerAsnLeuGluGlyGlnSerAspGluA
                                                                                                                                                                   1 GluGlnValSerHisGlyThrGlnAsnArgProLeuLeuArgAsnSerLe
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Lahive and Cockfield STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
GGATGATCTTGTTGGGCCACCTTCCAACCTGGAAGGCCAGAGTGACGAAA
                                                                                                                                                    GAACAAGTTTCTCATGGCACTCAAAATAGGCCTCTTCTTAGGAATTCCCT
                                                                                                                                                                                                                                                                                                                                                        Quality:
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: 5.216
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Gaps: 0
Percent Identity: 100.000
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                                                                                                                                                                                                                         from: 1 to:
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alignment_block:
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   Sequence 1, Application US/09513066
   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                               Quality: 845.00
Ratio: 5.216
Percent Similarity: 100.000
                                                                                                                                                          Align seg 1/1 to: US-09-513-066-1 from: 1 to: 4496
                                                                                                                                                                                                               US-09-041-994-2_COPY_1018_1179 x US-09-513-066-1
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SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Chen, J. Don
APPLICANT: Leo, Christopher
APPLICANT: Li, Hui
TITLE OF INVENTION: NOVEL USES FOR THE RAC3 TRANSCRIPTIONAL COACTIVATOR OF
TITLE OF INVENTION: STEROID NUCLEAR RECEPTORS
TILLE REFERENCE: UMG-026CP
CURRENT APPLICATION NUMBER: US/09/513,066
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: USSN 09/041,994
PRIOR PILING DATE: 1998-03-13
PRIOR APPLICATION NUMBER: USSN 60/073,674
PRIOR FILING DATE: 1998-02-04
NUMBER OF SEQ ID NOS: 37
CRETURER: DESCRIPTION NUMBER: USSN 60/073,674
PRIOR FILING DATE: 1998-02-04
NUMBER OF SEQ ID NOS: 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: CDS
LOCATION: (86)..(4330)
                                                    3137 GAACAAGTTTCTCATGGCACTCAAAATAGGCCTCTTCTTAGGAATTCCCCT 3186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 4496
TYPE: DNA
ORGANISM: Homo sapiens
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17 uAspAspLeuValGlyProProSerAsnLeuGluGlyGlnSerAspGluA 34
                                                                             1 GluGlnValSerHisGlyThrGlnAsnArgProLeuLeuArgAsnSerLe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAGCAACTTAGAATGCAGCTTCAGCAGAGGCTGCAG
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                                                                                                                                                                                                                                                                                               Percent Identity: 100.000
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seq_name: /cgn2_6/ptodata/1/pna/US6006_COMB.seq:US-60-068-511-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/60068511
GENERAL INFORMATION:
APPLICANT: Suen, Chen-Shian
APPLICANT: Frail, Donald E.
APPLICANT: Lyttle, Richard C.
TITLE OF INVENTION: Cloning and Expression of a Nuclear
TITLE OF INVENTION: Receptor Coactivator Proteins and Us
NUMBER OF SEQUENCES: 3
                                         TELEFAX: 973-683-4117
INFORMATION FOR SEQ ID NO: 1:
                                                       ATTORNEY/AGENT INFORMATION:
NAME: Walsh, Andrea C.
REGISTRATION UNMBER: 34 988
REFERENCE/DOCKET NUMBER: 972-
TELEOMYUNICATION INFORMATION:
TELEPHONE: 973-683-2169
TELEFAX: 973-683-4117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3187
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM CC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         117
SEQUENCE CHARACTERISTICS:
LENGTH: 4789 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  151
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                                                                                                                                                                                                                                                                                                                                                                                                  STATE: N
COUNTRY:
                                                                                                                                                                                              FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Parsippany
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
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                                                                                                                                                                                                                                         US/60/068,511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Products Corporation
                                                                                                                     97243-00
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STRANDEDNESS: single

TOPOLOGY:

linear

CDNA NO

; US-60-068-511-1

FEATURE:

NAME/KEY:

CDS 185..4750 MOLECULE TYPE: (
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:

ORGANISM: Homo sapiens

alignment_scores:

Quality: 845.00 Ratio: 5.216 Percent Similarity: 100.000

Percent Identity: 100.000

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                                                                                                                            seq_documentation_block:
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US-09-041-994-2_COPY_1018_1179 x US-60-068-511-1
                                                                                                                                                              seq_name: /cgn2_6/ptodata/1/pna/US094_COMB.seq:US-09-440-612-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: US-60-068-511-1 from: 1 to:
Sequence 1, Application US/09440612
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Lex M. Cowsert
TITLE OF INVENTION: ANYISENSE MODULATION OF SRC-3
FILE REFERENCE: RTS-0042
CURRENT APPLICATION NUMBER: US/09/440,612
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                                       EXPRESSION
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; NAME/KEY: CDS
; LOCATION: (184)..(4422)
US-09-440-612-1
                                                                                                          seq_documentation_block:
; Sequence 3, Applicatio
                                                                                                                                                       seq_name: /cgn2_6/ptodata/1/pna/US094_COMB.seq:US-09-440-612-3
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                                            GENERAL INFORMATION:
GENERAL INFORMATION:
C. Frank Bennett
APPLICANT: Lex M. Cowsert
TITLE OF INVENTION:
ANTISENS
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NUMBER OF SEQ ID NOS: 47
SEQ ID NO 1
LENGTH: 6754
FILE REFERENCE: RTS-0042
CURRENT APPLICATION NUMBER: US/09/440,612A
CURRENT FILING DATE: 1999-11-15
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ORGANISM: Homo
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                                                                                                            Application
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                                                 ANTISENSE MODULATION OF
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                                                 EXPRESSION
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seq_documentation_block:
    Sequence 1, Application US/09125635
; GENERAL INFORMATION:
    APPLICANT: THE UNITED STATES OF AMERICA represented by THE SE
; TITLE OF INVENTION: AIB1, A novel steriod receptor co-activator
; FILE REFERENCE: 49944
; CURRENT APPLICATION NUMBER: US/09/125,635
; CURRENT FILING DATE: 1998-08-21
; PRIOR APPLICATION NUMBER: 60/049,728
; PRIOR FILING DATE: 1997-06-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_block:
US-09-041-994-2_COPY_1018_1179 x US-09-440-612-3
                                                                                                                                                                                               seq_name:
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; LOCATION: (184)..(4422)
US-09-440-612-3
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SEQ ID N
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TYPE: DNA
ORGANISM: Homo s
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Ratio: 5.216
Similarity: 100.000
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; NAME/KEY: CDS
; LOCATION: (201)..(4463)
US-09-125-635-1
                                                                                                                                                seq_documentation_block:
                                                                                                                                                                                    seq_name: /cgn2_6/ptodata/1/pna/US093_COMB.seq:US-09-359-922-3962
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US-09-041-994-2_COPY_1018_1179 x US-09-125-635-1
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Sequence 3962, Application US/09359922
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL CONTIGS OBTAINER
TITLE OF INVENTION: LIBRARIES
FILE REFERENCE: 20411-752CON1
CURRENT APPLICATION NUMBER: US/09/359,922
CURRENT FILING DATE: 1999-07-22
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Ratio: 5.216
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo :
FEATURE:
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SOFTWARE: PatentIn Ver.
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                                                                                                                                                                                                                                                                                                                                                                                     rPheAsnSerMetAsnGlnMetAsnGlnGlnGlyAsnPheProLeuG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAGGGGCCTCCAATGCAAGGAGGCTTTCATCTTCAGGGACAATCACCATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GlnGlyProProMetGlnGlyGlyPheHisLeuGlnGlyGlnSerProSe 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAGCATTATTGGACCAGCTGCACACTCTTCTCAGCAACACAGATGCCACA
                                                                                                                                                                                                                                                                                             AAGGAATGCACCCACGAGCCAACATCATGAGACCCCGGACAAACACCCCCC
                                                                                                                                                                                                                                                                                                                                                                TTTTAACTCTATGATGAATCAGATGAACCAGCAAGGCAATTTTCCTCTCC
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                                                                            OBTAINED
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                                                                            FROM VARIOUS
                                                                            CDNA
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seq_documentation_block:
; Sequence 3962, Applica
; GENERAL INFORMATION:
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NAME/KEY: misc_feature

LOCATION: (1)...(6855)

OTHER INFORMATION: n =

US-09-359-922-3962
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                                                                                                                                     seq_name: /cgn2_6/ptodata/1/pna/US093_COMB.seq:US-09-359-922-3962
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: US-09-359-922-3962 from: 1 to: 6855
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EARLIER APPLICATION NUMBER: US 09/205,155
EARLIER FILING DATE: 1998-12-03
NUMBER OF SEQ ID NOS: 13203
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 3962
APPLICANT: Leshkowitz, Dena
APPLICANT: Liu, Jin
TITLE OF INVENTION: NOVEL CONTIGS OBTAINED FROM VARIOUS CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                                                 LysGlnLeuArgMetGlnLeuGlnGlnArgLeuGln 162
                                                                                                                                                                                                                                                                          lnGlyMetHisProArgAlaAsnIleMetArgProArgThrAsnThrPro 150
                                                                                                                                                                                                                                                                                                                                                         rPheAsnSerMetAsnGlnMetAsnGlnGlnGlyAsnPheProLeuG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGCCTGGAAGAATTGACAGAGCTTTGGGCATTCCTGAACTTGTCAATCA 3451
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                                                                                                                                                                                                                                                                                                                                     TTTTAACTCTATGATGAATCAGATGAACCAGCAAGGCAATTTTCCTCTCC
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                                                                                                                                                                                                                                                        AAGGAATGCACCCACGAGCCAACATCATGAGACCCCCGGACAAACACCCCC
                                                                                                                                                                             AAGCAACTTAGAATGCAGCTTCAGCAGAGGCTGCAG 3737
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                                                                            Application US/09359922A
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Percent Identity: 100.000
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FEATURE:

NAME/KDY: misc_feature

LOCATION: (1)...(6855)

OTHER INFORMATION: n = A

US-09-359-922-3962
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US-09-041-994-2_COPY_1018_1179 x US-09-359-922-3962
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    Quality:
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LENGTH: 6855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/359,922A CURRENT FILING DATE: 1999-07-22 EARLIER APPLICATION NUMBER: US 09/205,155 EARLIER FILING DATE: 1998-12-03 EARLIER APPLICATION NUMBER: US 09/034,341 EARLIER FILING DATE: 1998-02-13 NUMBER OF SEQ ID NOS: 13203 NUMBER: FastSEQ for Windows Version 3.0 SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: 20411-752CON1
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                  101 GlnGlyProProMetGlnGlyGlyPheHisLeuGlnGlyGlnSerProSe 117
                                                                                                                                                                                                                                                                                                        84 laValMetMetAspGlnLysAlaGlyLeuTyrGlyGlnThrTyrProAla 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      51 GlyLeuGluGluIleAspArgAlaLeuGlyIleProGluLeuValAsnGl 67
                                                                                                                                          GGGACAGGCATTAGAGCCCAAACAGGATGCTTTCCAAGGCCAAGAAGCAG 3501
                                                                                                                                                                                                                                                                                                                                                                               nGlyGlnAlaLeuGluProLysGlnAspAlaPheGlnGlyGlnGluAlaA 84
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                                                                   AAGCAACTTAGAATGCAGCTTCAGCAGAGGCTGCAG 3737
                LysGlnLeuArgMetGlnLeuGlnGlnArgLeuGln
                                                                                                                                                                                rPheAsnSerMetMetAsnGlnMetAsnGlnGlnGlyAsnPheProLeuG 134
                                                                                                                                                                                                                  CAGGGGCCTCCAATGCAAGGAGGCTTTCATCTTCAGGGACAATCACCATC
                                                                                                       lnGlyMetHisProArgAlaAsnIleMetArgProArgThrAsnThrPro
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5.216
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Gaps:
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/cgn2_6/ptodata/1/pna/US6020_COMB.seq:US-60-209-009-198

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seq_documentation_block:
Sequence 198, Application US/60209009
GENERAL INFORMATION:
APPLICANT: Faris, Mary
APPLICANT: Pearson, Cecelia I.
TITLE OF INVENTION:
FILE REFERENCE: PA-0027 P
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Quality:
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Ratio: 5.216
Percent Similarity: 100.000
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CURRENT FILING DATE: 2000-06-01
NUMBER OF SEQ ID NOS: 501
SOFTWARE: PERL Program
SEQ ID NO 198
LENGTH: 7116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Incyte ID NO: 1094199.1 NAME/KEY: unsure LOCATION: 3941-3993, 5899-5939, 6951 OTHER INFORMATION: a, t, c, g, or other :-60-209-009-198
 3702
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3352 GAGCATTATTGGACCAGCTGCACACTCTTCTCAGCAACACAGATGCCACA 3401
             151 LysGlnLeuArgMetGlnLeuGlnGlnArgLeuGln 162
                                                                                                 134
                                                                                                                                                                                                84 laValMetMetAspGlnLysAlaGlyLeuTyrGlyGlnThrTyrProAla 100
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                                                                                                                                 nGlyGlnAlaLeuGluProLysGlnAspAlaPheGlnGlyGlnGluAlaA 84
 AAGCAACTTAGAATGCAGCTTCAGCAGAGGCTGCAG
                                                              AAGGAATGCACCCACGAGCCAACATCATGAGACCCCGGACAAACACCCCC
                                                                                                                                                                rPheAsnSerMetMetAsnGlnMetAsnGlnGlnGlyAsnPheProLeuG
                                                                                                                                                                                                                                                                  GGGACAGGCATTAGAGCCCAAACAGGATGCTTTCCAAGGCCAAGAAGCAG
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Percent Identity: 100.000
3737
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APPLICANT: Morris, MacDonald
APPLICANT: Lal, Preeti
APPLICANT: Diep, Dinh
ITILE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
ITILE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
ITILE OF INVENTION: Identified Thereby
ITILE OF INVENTION: Identified Thereby
ITILE OF INVENTION: Identified Thereby
ITILE OF INVENTION: UNMBER: US/60/213,360
CURRENT APPLICATION NUMBER: US/60/213,360
CURRENT FILING DATE: 2000-06-21
NUMBER OF SEQ ID NOS: 8347
SOFTWARE: PERL Program
SQT ID NO 7991
LENGTH: 7116
TYPE: DNA
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_block:
US-09-041-994-2_COPY_1018_1179 x US-60-213-360-7991
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; LOCATION: 3941-3993, 5899-5939, 6951

; OTHER INFORMATION: a, t, c, g, or ot

US-60-213-360-7991
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Ratio: 5.216
Percent Similarity: 100.000
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134 lnGlyMetHisProArgAlaAsnIleMetArgProArgThrAsnThrPro
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                                                                             rPheAsnSerMetAsnGlnMetAsnGlnGlnGlyAsnPheProLeuG 134
                                                                                                                                                  CAGGGGCCTCCAATGCAAGGAGGCTTTCATCTTCAGGGACAATCACCATC
                                                                                                                                                                         GlnGlyProProMetGlnGlyGlyPheHisLeuGlnGlyGlnSerProSe
                                                                                                                                                                                                                                                                                                                                                 nGlyGlnAlaLeuGluProLySGlnAspAlaPheGlnGlyGlnGluAlaA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAGCATTATTGGACCAGCTGCACACTCTTCTCAGCAACACAGATGCCACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGATGATCTTGTTGGGCCACCTTCCAACCTGGAAGGCCAGAGTGACGAAA
                                                   TTTTAACTCTATGATGAATCAGATGAACCAGCAAGGCAATTTTCCTCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGCCTGGAAGAATTGACAGAGCTTTGGGCATTCCTGAACTTGTCAATCA
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Percent Identity:
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alignment_block:
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Ratio: 5.216
Percent Similarity: 100.000
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GENERAL INFORMATION:
APPLICANT: Holtzman Down 1
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SEQ ID NO 8947
LENGTH: 7888
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TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.1186-001
CURRENT APPLICATION NUMBER: US/09/652,123
CURRENT FILING DATE: 2000-08-30
PRIOR APPLICATION NUMBER: 60/151,135
PRIOR APPLICATION NUMBER: 60/151,135
PRIOR FILING DATE: 1999-08-30
NUMBER OF SEQ ID NOS: 9796
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134 lnGlyMetHisProArgAlaAsnIleMetArgProArgThrAsnThrPro
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                                                                                                                                  CAGGGGCCTCCAATGCAAGGAGGCTTTCATCTTCAGGGACAATCACCATC
                                                       TTTTAACTCTATGATGAATCAGATGAACCAGCAAGGCAATTTTCCTCTCC
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alignment_block:
us-09-041-994-2_COPY_1018_1179 x us-09-652-127-9831
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Quality:
Ratio:
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; ORGANISM: HOMO
US-09-652-127-9831
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Sequence 9831, Applica:
GENERAL INFORMATION:
APPLICANT: Shyjan, A
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TITLE OF INVENTION: NOVEL NUCLEIC ACID MOL
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.1183-001
CURRENT APPLICATION NUMBER: US/09/652,127
CURRENT FILING DATE: 2000-08-30
PRIOR APPLICATION NUMBER: 60/151,134
PRIOR FILING DATE: 1999-08-30
PRIOR FILING DATE: 1999-08-30
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SOFTWARE: FastSEQ for
SEQ ID NO 9831
LENGTH: 7888
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                                                                                                                                                                                                101 GlnGlyProProMetGlnGlyGlyPheHisLeuGlnGlyGlnSerProSe 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        51 GlyLeuGluGluIleAspArgAlaLeuGlyIleProGluLeuValAsnGl
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rPheAsnSerMetMetAsnGlnMetAsnGlnGlnGlyAsnPheProLeuG
                                                                                                                                                                              CAGGGGCCTCCAATGCAAGGAGGCTTTCATCTTCAGGGACAATCACCATC
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5.216
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NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for WI
SEQ ID NO 11058
LENGTH: 7888
TYPE: DNA
ORGANISM: Homo sapiens
US-09-652-355-11058
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Quality:
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; Sequence 11058, Applic
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TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLI
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.1192-001
CURRENT APPLICATION NUMBER: US/09/652,355
CURRENT FILING DATE: 2000-08-30
PRIOR APPLICATION NUMBER: 60/151,136
PRIOR APPLICATION NUMBER: 60/151,136
PRIOR FILING DATE: 1999-08-30
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Ratio: 5.216
Percent Similarity: 100.000
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rPheAsnSermetMetAsnGlnMetAsnGlnGlyAsnPheProLeuG
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                                                                                                                                    GGGACAGGCATTAGAGCCCAAACAGGATGCTTTCCAAGGCCAAGAAGCAG
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Percent Identity: 100.000
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alignment_block:
US-09-041-994-2_COPY_1018_1179 x US-09-663-693-1028
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 1028
: LENGTH: 7888
; LENGTH: 7888
; TYPE: DNA
; ORGANIZM: Homo Sapiens
US-09-663-693-1028
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Ratio: 5.216
Percent Similarity: 100.000
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TITLE OF INVENTION: MOVEL NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.1195-001
CURRENT APPLICATION NUMBER: US/09/663,693
CURRENT FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: 60/154,986
PRIOR PILING DATE: 1999-09-21
PRIOR PILING DATE: 1999-09-21
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                         lnGlyMetHisProArgAlaAsnIleMetArgProArgThrAsnThrPro 150
                                                                                                                                             rPheAsnSerMetAsnGlnMetAsnGlnGlnGlyAsnPheProLeuG 134
                                                                                                                                                                                                 CAGGGGCCTCCAATGCAAGGAGGCTTTCATCTTCAGGGACAATCACCATC 3567
                                                                                                 TTTTAACTCTATGATGAATCAGATGAACCAGCAAGGCAATTTTCCTCTCC
AAGGAATGCACCCACGAGCCAACATCATGAGACCCCGGACAAACACCCCC
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LysGlnLeuArgMetGlnLeuGlnGlnArgLeuGln 162

3668 AAGCAACTTAGAATGCAGCTTCAGCAGAGGCTGCAG 3703

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APPLICANT: Gearing, David P.
APPLICANT: Gearing, Douglas A.
APPLICANT: Kingsbury, Gillian A.
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND TITLE OF INVENTION: THEREFOR FILE REFERENCE: 1600.2014-001
CURRENT APPLICATION NUMBER: US/09/698,014
CURRENT FILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: 60/162,363
PRIOR APPLICATION NUMBER: 50/162,363
PRIOR APPLICATION NUMBER: 50
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US-09-041-994-2_COPY_1018_1179 x US-09-698-014-5135
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    Sequence 5135, Application US/09698014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_name: /cgn2_6/ptodata/1/pna/US096E_COMB.seq:US-09-698-014-5135
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Ratio: 5.216
Percent Similarity: 100.000
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APPLICANT: Gearing,
APPLICANT: Holtzmar
                                                                                                                                                                         3568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3218 GAACAAGTTTCTCATGGCACTCAAAATAGGCCTCTTCTTAGGAATTCCCT 3267
                                                                                                                                                                                                                                                                                                                                               3518 CAGGGGCCTCCAATGCAAGGAGGCTTTCATCTTCAGGGACAATCACCATC 3567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     134 lnGlyMetHisProArgAlaAsnIleMetArgProArgThrAsnThrPro 150
                                                                                                                                                                                                                      117 rPheAsnSerMetMsnGlnMetAsnGlnGlnGlyAsnPheProLeuG 134
                                                                                                                                                                                                                                                                                                                                                                                            101 GlnGlyProProMetGlnGlyGlyPheHisLeuGlnGlyGlnSerProSe .117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84 laValMetMetAspGlnLysAlaGlyLeuTyrGlyGlnThrTyrProAla 100
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AAGGAATGCACCCACGAGCCAACATCATGAGACCCCGGACAAACACCCCC
                                                                                                                                                                         TTTTAACTCTATGATGAATCAGATGAACCAGCAAGGCAATTTTCCTCTCC
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Gaps: 0
Percent Identity: 100.000
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3667

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of: US-09-041-994-2_COPY_1018_1179

to: Pending_Patents_NA_New:*

out_format :

pfs

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Database: Pending_Patents_NA_New:* Database sequences: 201016
Database length: 146721182
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Query: US-09-041-994-2_COPY_1018_1179
Query length: 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Search time (sec): 114.180000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:US-09-196-29
/cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:US-09-540-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -Q=/cgn2_1/USFTO_Spool/US09041994/runat_30042001_165632_19523/app_query.fasta_1.1940
-DB=-Pending_Patents_NA_New -OFMT=fastap_-SUFFIX=p2n.rnpn
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-XGAPEXT=0.000 -FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000
-YGAPEXT=0.500 -DELOP=6.000 -DELEXT=7.000 -YGAPOP=10.000
-YGAPEXT=0.500 -DELOP=6.000 -DELEXT=7.000 -START=1
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-NATRIX=blosum62 -TRANS=human40.cd1=7.000-START=5
-OUTEMT=pfs -NORM=ext -MINLEN=0 -MAXLEN=200000000
-USER=US09041994_@CGN1_1_175 -NCPU=6 -ICPU=3 -LONGLOG -NO_XLPXY
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Compugen Ltd.
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seq_documentation_block:
; Sequence 1, Application
; GENERAL INFORMATION:
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Ratio: 5.216
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/196,296B
CURRENT FILING DATE: 1998-11-19
NUMBER OF SEQ ID NOS: 3
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Suen, Chen-Shian
APPLICANT: Frail, Donald E.
APPLICANT: Lyttle, Richard C.
TITLE OF INVENTION: Cloning and Expression of a Nuclear
TITLE OF INVENTION: Receptor Coactivator Proteins and (FILE REFERENCE: 0630/01376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 4789
TYPE: DNA
ORGANISM: Homo S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3236 GAACAAGTTTCTCATGGCACTCAAAATAGGCCTCTTCTTAGGAATTCCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34 rgAlaLeuLeuAspGlnLeuHisThrLeuLeuSerAsnThrAspAlaThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GluGlnValSerHisGlyThrGlnAsnArgProLeuLeuArgAsnSerLe
                                                                                                                       lnGlyMetHisProArgAlaAsnIleMetArgProArgThrAsnThrPro 150
                                                                                                                                                                                             rPheAsnSerMetMetAsnGlnMetAsnGlnGlnGlyAsnPheProLeuG
                                                   TTTTAACTCTATGATGAATCAGATGAACCAGCAAGGCAATTTTCCTCTCC
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2.2e+04
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151 LysGlnLeuArgMetGlnLeuGlnGlnArgLeuGln 162

AAGCAACTTAGAATGCAGCTTCAGCAGAGGCTGCAG 3721

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; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No:
US-09-540-212A-48616
                                                                                                                                                                                                   seq_documentation_block:
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US-09-041-994-2_COPY_1018_1179 x US-09-540-212A-48616
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/540,212A
CURRENT FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 67551
SOFTWARE: PERL Program
SEQ ID NO 48616
LENGTH: 274
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                Sequence 387, Application US/60248505 GENERAL INFORMATION:
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                     APPLICANT: Beasley, Ellen
TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
FILE REFERENCE: c1000918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Mullahy, Sara J.

APPLICANT: Naughton, Rebecca E.

TITLE OF INVENTION: POLYNUCLEOTIDES OF AIRWAY AND FILE REFERENCE: PD-1034 CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Seilhamer, Jeffrey J.
APPLICANT: DeLegeane, Angelo M.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuve, Laura L.
  CURRENT APPLICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                            224
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                                                                                                                                                                                                                                                                                                                                                      99 oAlaGlnGlyPro.....ProMetGlnGly 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68 lyGlnAlaLeuGluProLysGlnAspAlaPheGlnGlyGlnGluAlaAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51 yLeuGluGluIleAspArgAlaLeuGlyIleProGluLeuValAsnGlnG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77 GCTAGCTGAACTAGACAGAGCTCTGGGAATTGACAAACTTGTT...CAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27 GCTCTTCTTGAACAGCTGGTATCCTTCCTTAGTGGCAAAGTTGAAACTGA 76
                                                                                                                                                                                                                                                                                                                                                                                                           CCACCTTTGATCATGGAAGAAAGACCCAACCTTTATTCCCAGCCTTACTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGGGTGGATTAGATGTATTATCAGAGAGATTTCCACCACAACAAGCAACG
                                                                                                                                                                                                                                                                                                         TTCTCCTTCTCCTACTGCCAATCTCCCTAGCCCTTTCCAAGGC 266
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2.245
67.901
NUMBER: US/60/248,505
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Percent Identity: 40.741
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alignment_scores:
Quality:
Ratio:
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; ORGANISM: human
US-60-248-505-387
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US-09-041-994-2_COPY_1018_1179 x US-60-248-505-387
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NUMBER OF SEQ ID NOS: 1
SOFTWARE: FastSEQ for v
SEQ ID NO 387
LENGTH: 5132
; NUMBER OF SEQ ID NOS: J
SOFTWARE: FASTSEQ for V
SEQ ID NO 222
LENGTH: 31818
; TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                            seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq:US-60-248-505-222
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                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Beasley, Ellen
                                                                                                                                                                                                                                                                                                                                  Sequence 222,
                                                                                                                         TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULI TITLE OF INVENTION: PROTEINS, AND USES THEREOF FILE REFERENCE: C1000918

CURRENT APPLICATION NUMBER: US/60/248,505

CURRENT FILING DATE: 2000-11-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3541 CCGCTCCCGCTCTCAGCCAGAAGCTGCGCTGGGCACTCGGGAGAAAGCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3641 CCGGGTGGCAGCTAT.....AGGGAACCAGGCTTCGGAAGTCTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   107 ...GlyGlyPheHisLeuGlnGlyGlnSerProSerPheAsnSerMetMe 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   139 rgAlaAsnIleMetArgProArg
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                                                                                                                                                                                                                                                                                                                                       Application US/60248505
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                                                                               Windows Version 4.0
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seq_documentation_block:
    Sequence 6007, Application US/09739449
    GENERAL INFORMATION:
    APPLICANT: Hinkle, Gregory J.
    APPLICANT: Slater, Steven C.
    TITLE OF INVENTION: Agrobacterium tumefaciens Gen
    FILE REFERENCE: 38-10(15490)C
    CURRENT APPLICATION NUMBER: US/09/739,449
    CURRENT FILING DATE: 2000-12-19
    PRIOR APPLICATION NUMBER: US 09/514,000
    PRIOR APPLICATION NUMBER: US 09/514,000
    PRIOR FILING DATE: 2000-02-23
    NUMBER OF SEQ ID NOS: 13351
    SEQ ID NO 6007
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US-09-041-994-2_COPY_1018_1179 x US-60-248-505-222
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US-60-248-505-222
                        alignment_scores:
                                                                                                   ; ORGANISM: Agrobacterium tumefaciens US-09-739-449-6007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:US-09-739-449-6007
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                                                                                                                                                    TYPE: DNA
                                                                                                                                                                              LENGTH: 2349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AG.....CGGGCTCTCGGCCTCGGCCCAGGCCAGGGCCAGGGGCT 30176
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Quality:
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168
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seq_documentation_block:
; Sequence 217, Application US/09739449
; GENERAL INFORMATION:
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US-09-041-994-2_COPY_1018_1179 x US-09-739-449-6007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:US-09-739-449-217
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Percent Similarity:
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                                                                                                                  SEQ ID NO 217
LENGTH: 397803
                                                                                                                                                                                                                                    APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15490)C
CURRENT APPLICATION NUMBER: US/09/739,449
CURRENT FILING DATE: 2000-12-19
                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 09/514,000 PRIOR FILING DATE: 2000-02-23 NUMBER OF SEQ ID NOS: 13351
  NAME/KEY:
                                                                TYPE: DNA ORGANISM: Agrobacterium
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                                                 FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  uGln 158
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Percent Identity:
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seq_documentation_block:
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US-09-041-994-2_COPY_1018_1179 x US-09-739-449-217
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                                                                                                                                                                                                                                                                                                                                                seq_name: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:US-09-654-935A-99
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                                                                                                                                                                         Sequence 99, Application US/09654935A
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Zhou, Ping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: US-09-739-449-217 from: 1 to: 397803
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                                                                                                                              APPLICANT:
APPLICANT:
                                                                                 APPLICANT:
                                                          APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31912
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31812 GCGAAATTCTTCAGCAGCAGCAGAAGTTGATGGACGAGACTTTCAAGCTC 31861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31762 GCAGGGACAGCAACAGAGCAGCAAGATGCGCCAGCAGATCGACAAGCTGG 31811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31630 TCTGGAAAACATGATGAACCAGATCGAGAACCTTGCCCGTTCCGGCAATC 31679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31580 CCCCAAGCCAACATGAACAACCAAGCCCAGAACGTGCTGCGCCAGCGCGA 31629
            APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              142 IleMetArgProArgThrAsn...ThrProLysGlnLeuArgMetGlnLe 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hraspalaThrGly.....LeuGluGluIleAspargalaLeuGlyIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ProGluLeuValAsnGlnGlyGlnAlaLeuGluProLySGlnAspAlaPh 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTGACGCGCGCAGGAAATGCTCTCGCAGCTACAGCGC......
                                                                                                                                                                                                                                                                                                                                                                                                     GAAA 32065
                                                                                                                                                                                                                                                                                                                                                                                                                                                      uGln 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAGGCCAGCAAGGTCAACCGGGTCAACAAGGCCAGAATGGTCAGCAGGGC 32011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            etAsnGlnGlnAsnPheProLeuGlnGlyMetHisProArgAlaAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGAAGGCGAAGACGAGCAGCAGATGGGCGAGAATGGCCAGCCGCCACAGG 31961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          yPheHisLeuGlnGlyGlnSerProSerPheAsnSerMetMetAsnGlnM 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ......GlyProProMetGlnGlyGl 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lyGlnThrTyrProAlaGln.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     eGlnGlyGlnGluAlaAlaValMetMetAspGlnLysAlaGlyLeuTyrG 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ....ATGATGAACAATCTGCAGGCTGGCCGCCGCCAGCGGCAAGGCCA 31761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pGluArgAlaLeuLeuAspGlnLeuHisThrLeuLeu.....SerAsnT 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ProProSerAsnLeuGluGlyGlnSer.....As
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality:
                           Zhang, Jie
Zhao, Qing A.
Xue, Aidong J.
                                                                                                  Asundi, Vinod
Wang, Jian-Rui
Ren, Feiyan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ratio:
            Wehrman, Tom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92.00
1.045
52.381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31911
seq_documentation_block:
    Sequence 12214, Application US/09335032
    GENERAL INFORMATION:
    APPLICANT: Velculescu, Victor
    APPLICANT: Vogelstein, Bert
    APPLICANT: Kinzler, Kenneth
    TITLE OF INVENTION: Characterization of the
    TITLE OF INVENTION: Transcriptome
    FILE REFERENCE: 01107.78572
    CURRENT APPLICATION NUMBER: US/09/335,032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality:
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APPLICANT: Wang, Zhiwei
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: Novel Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 793
CURRENT APPLICATION NUMBER: US/09/654,935A
CURRENT FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 271
SOFTWARE: DL_FL_genes Version 1.0
SEQ ID NO 99
LENGTH: 12279
TYDE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_block:
US-09-041-994-2_COPY_1018_1179 x US-09-654-935A-99/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; NAME/KEY: CDS
; LOCATION: (8405)..(12226)
US-09-654-935A-99
seq_name: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:US-09-335-032-12214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to reverse of: US-09-654-935A-99 from: 1
                                                            11576 GCTCCAGGCAGCTCAGCACATCCGGGGC 11549
                                                                                                                                                                                                                                                                                   11676 ATGAGCTTCAGCTGCAGCAGGAAGGAGGAGACGCCGCTGTACTTGCTCAG
                                                                                                                                                                                                                                                                                                                                                                                                  11726 GCAGGGCTGTGCGCTTGAGGTGGAAGCAGACGTCCTTGAGCGCCCACATC 11677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11767 CTGCAGCTGACGGAACTGCACAGAGCC.......GGCCATGTGGCTCA 11727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11815 ..GTAGCCCTGGATGACCTTCACGAAATGCTGCATCTCGTGCTTGAACAG 11768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11834 GCAGGATCTGGTTGGCGAT..... 11816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11884 CAGGTCGCCCACGGTGGCCCAACCTGGCCCCTGAACTCGCACCAGGTGACGT 11835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17 uAspAspLeuValGlyProProSerAsnLeuGluGlyGlnSerAspGluA ::::||||||||||||
                                                                                                                                                                                                                                                                                                                                                                                                                                             50 ThrGlyLeuGluGluIleAspArgAlaLeuGlyIleProGluLeuValAs 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34 rgAlaLeuLeuAspGlnLeuHisThrLeuLeuSerAsnThr...AspAla 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 GlnValSerHisGlyThrGlnAsnArgPro...LeuLeuArgAsnSerLe
                                                                                                                                                                     GCAGCCCTCGGTGATGACAATGTTGAGAGGCCAGTCCACCTTGTACCTGA 11577
                                                                                                                 oMetGlnGlyGlyPheHisLeuGlnGly
                                                                                                                                                                                                                            GlnLysAlaGlyLeuTyrGlyGlnThrTyrProAlaGln...GlyProPr 104
                                                                                                                                                                                                                                                                                                                                           86.00
1.284
53.175
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Gaps: 6
Percent Identity: 28.571
                                                                                                                    113
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of the Yeast

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seq_documentation_block:
    Sequence 6422, Application US/09801833
    GENERAL INFORMATION:
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US-09-041-994-2_COPY_1018_1179 x US-09-335-032-12214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_scores:
Quality:
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US-09-335-032-12214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: US-09-335-032-12214 from: 1 to: 666448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            365901 GAGCAGTTGTCTTATAACACCGTTCAACAGTCTCCCATAACGAATAAACA 365950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 12214
LENGTH: 666448
                                                                                                                                                                                                                                                                              366333
                                                                                                                                                                                                                                                                                                                                                                                   366301 GTTTTCATTCT......AGACAAGGATCAGTCGCCAGC 366332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   366251 GCAACCGTACAACCCATCGATATCATCTTTTGGCCAGTTCGCTGCTAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                366201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       366001 CCTCTGGTAGTGGTGGTTATTGGTCCTTTATAAGAACTTCTGGTTTACTA 366050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    365951 TACTAATGATTCTGGAAATGCAAACGGAAGTGTCACCGGCTCAGGCAGTG 366000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT FILING DATE: 1999-06-16
PRIOR APPLICATION NUMBER: US 60/035,917
PRIOR FILING DATE: 1997-01-23
PRIOR APPLICATION NUMBER: US 09/012,031
PRIOR FILING DATE: 1998-01-22
NUMBER OF SEQ ID NOS: 12219
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAGTTGCAACAAGGACAGAACCTATACTCGTATTCTCAATTTTCCCAGCA 366250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCTCCTACTGATGATCATAATGGGGAACAGACAAGAAGATCAAGTTCCAT 366100
                                                                                                                                                                                                                                                                        GAGGCTATGTCTCCCAGTGCACCTGCCATGTTTACTAGCACATCTACAAA
                                                                                                                                                                                                                                                                                                                            GlnGlyMetHisProArgAlaAsnIleMetArgProArgThrAsnThr.. 149
                                                                                                                                                                                                                                                                                                                                                                                                                                         {\tt erPheAsnSerMetMetAsnGlnMetAsnGlnGlnGlyAsnPheProLeu}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MetMetAspGlnLysAlaGlyLeuTyrGlyGlnThrTyrProAlaGlnGl 102
::::::||| ::: ::: :::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTCAGCTTCCCCCACCTCAGCAACAATCGCAGCCACAAGCACCAACAA 366200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SerAsnThrAspAlaThrGlyLeuGluGluIleAspArgAlaLeuGlyIl 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rLeuAspAspLeuValGlyProProSerAsnLeuGluGlyGln..... 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              yProProMetGlnGlyGlyPheHisLeuGlnGlyGln.....SerProS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCTTCTTTGCTACGAAATACTTCAAATTCTCTTTTACTAGGTGGCCAGC 366150
                                                                                                                                                                 CCCCGTAAATGTTGCACAGCAAACACAAAGA 366413
                                                                                                                                                                                                                 .ProLysGlnLeuArgMetGlnLeuGlnGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..AlaLeuGluProLysGlnAspAlaPheGlnGlyGlnGluAlaAlaVal 85
                                                                                                       /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:US-09-801-833-6422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SerAspGluArgAlaLeuLeuAspGlnLeuHisThr.....LeuLeu 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.884
53.672
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Gaps: 8
Percent Identity: 25.989
                                                                                                                                                                                                                       159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          177
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alignment_block:
US-09-041-994-2_COPY_1018_1179 x US-09-801-833-6422/rev
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    Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; LOCATION: (1)...(2055)
; OTHER INFORMATION: n = A,T,C
US-09-801-833-6422
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Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/103,145
PRIOR FILING DATE: 1998-10-05
NUMBER OF SEO ID NOS: 8285
SOFTWARE: FASTSEQ for Windows Version
SEO ID NO 6422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/801, CURRENT FILING DATE: 2001-03-13 PRIOR APPLICATION NUMBER: 09/371,168 PRIOR FILING DATE: 1999-08-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/095,907 PRIOR FILING DATE: 1998-08-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Glucksmann, M. Alexandra
TITLE OF INVENTION: NUCLEIC ACID MOLECUL
TITLE OF INVENTION: HUMAN BRAIN LIBRARY
FILE REFERENCE: 1600.1037-005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PEATURE:
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              975
                      156
                                                              652
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                925 GCCCAGCCTGCGCTGTTGCCCTGAGGGCCGCCCTCGCCACTGCCCCG 876
                                                                                                                                                                                                                                                                                                                                              97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66 AsnGlnGly.....GlnAlaLeuGluProLysGlnAspAlaPheGlnGl 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22 GlyProProSerAsnLeuGluGlyGlnSerAspGluArgAlaLeuLeuAs
nLeuGlnGlnArgLeuGln 162
                                                                                                                                                                                                                                                                                                                           hrTyrProAlaGlnGlyProProMetGlnGlyGlyPheHisLeuGlnGly 113
                                                                                                                                         AGAGGAAGCGCCGAGAGGCACAGGTGGAGAAGTCGGGCTTCACCACACAG
                                                                                                                                                                                                                         AAAGACGTGAGCCGCCAGACAAGAGAAGCAGATGGCGAACAGAACCCCCAA
                                                                                                                                                                                                                                                          GlnSerProSerPheAsnSerMetAsnGlnMetAsnGln.....
                                                                                                                                                                                                                                                                                                      ATCACCCAGCCCCGGGGCCCGTGGTTCTTCCGGGCCAGGAAGTTGAGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                       yGlnGluAlaAlaValMetMetAspGlnLysAlaGlyLeuTyrGlyGlnT 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGAGTGCCATGACAAAGTCCATGTTGGCGATGGCACAGGGGGAGGCCACG
                                                              TCAGCAGCAGAGC......CACAGTGAAG 803
                                                                                                AlaAsnIleMetArgProArgThrAsnThrProLysGlnLeuArgMetGl 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ....LeuGluGluIleAspArgAlaLeuGlyIleProGluLeuVal
                                                                                                                                                                             2055
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1.038
49.682
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Percent Identity: 22.293
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GGTCCCCAGCAGGCTCCGT

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alignment_scores:
    Quality:
    Ratio:
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; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US01-09226-10
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TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP50018
CURRENT APPLICATION NUMBER: PCT/US01/09226
CURRENT FILING DATE: 2001-03-22
PRIOR APPLICATION NUMBER: 60/192.158
PRIOR APPLICATION NUMBER: 60/192.668
PRIOR APPLICATION NUMBER: 60/192.668
PRIOR FILING DATE: 2000-03-27
PRIOR FILING DATE: 2000-03-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-041-994-2_COPY_1018_1179 x PCT-US01-09226-10/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
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GENERAL INFORMATION:
APPLICANT: SMITHKLINE BEECHAM CORPORATION
APPLICANT: SMITHKLINE BEECHAM D.1.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version SEQ ID NO 10\,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/200,166
PRIOR FILING DATE: 2000-04-27
NUMBER OF SEQ ID NOS: 66
                                                                                                                                                                                                             1067
                                                                                                                                                                                                                                                                                                                                                                                                                                    1111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1211 ACGATCCAGCACACCGCGGGGGCCGAGCCCAGCTGGAACAGGGCCGCGTT 1162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1261 TGGGGACCGGGTCCTCCCCCTTCTCCATCTGCAGCTTCAGAGTCGTGCAC 1212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1311 GAACCGGCTGCAGAGGAAACGCAGGAACAGCCCCGTGCGGGTGAGGCAGG 1262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1161 GCTCCTCATTAGCTCAAAGGCACGCATGGCTTGGTCCTCGTCTCCAAAGT 1112
                                                                                                                                                                                                                                                                                                                                                                        72 luProLysGlnAspAlaPheGlnGlyGlnGluAlaAlaValMetMet... 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GluGlnValSerHisGlyThrGlnAsnArgProLeuLeuArgAsnSerLe 17
                                                                                                                                                                                                                                                                                                                                                                                                                                 GTCTCAGGAAATAGGCCCTCCTGTCCTCCTCCAG.....GAAGCCCTCC 1068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    eAspArgAlaLeuGlyIleProGluLeuValAsnGlnGlyGlnAlaLeuG 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .....AspGluArgAlaLeuLeuAspGln.......
  TCCCCGCAGATGTCCTCGATCAGCGCCCCAGGTGCGGCTCCCAGCTCATC
                                                                                                     TGTTCAGCAAACTCCCCAGGAGGACGGGCACCGGCTTCTTCTTCTCCCAG
                                                                                                                                                        oAlaGlnGlyProProMetGlnGlyGlyPheHisLeu.....
                                                                                                                                                                                                                                                                                                                         ACCCTTATGTAGATCGGCTCCTCCGCCAGGATCCGGAGGTCCCTCAGGGC
                                               .....AspGlnLysAlaGlyLeuTyrGlyGlnThrTyrPr 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ...LeuHisThrLeuLeuSerAsnThrAspAlaThrGlyLeuGluGluIl 55
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0.958
51.534
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Gaps: 7
Percent Identity: 25.767
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6
871
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alignment_block:
US-09-041-994-2_COPY_1018_1179 x PCT-US01-08117-154
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; OTHER INFORMATION: Incyte ID No: 1871961CB1
PCT-US01-08117-154
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CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 214
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TITLE OF INVENTION: TRANSCRIPTION FACTORS
FILE REFERENCE: PF-0761 PCT
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TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                    1027 ACGATTCCAGCCACGGGTCCTGCAGGTCCAGGCCCAGGTGCAGTCA.... 1072
                                                                                                                                                                                                                                                                 1073 .... CAGACTCAGCCGCGGATACCATCCACAGAC...ACCCAGGTGCAG
1191 AGCTGCAGCAGGAGGCAGAGCCACAGAAGCAGGTGCAGCCA......
                                                                                       1141 ACAGACCTCTCCAGAGCACTTAGTGCTGCAACAGAAGCAGGTGCAGCCAC
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                                                                                                                              a...LeuGluProLysGlnAspAlaPheGlnGlyGlnGluAlaAlaValM 86
                                                                                                                                                                                                                                                                                                           euAspGlnLeuHisThrLeuLeuSerAsnThrAspAlaThrGlyLeuGlu 53
                                         etMetAspGlnLysAlaGlyLeuTyrGlyGlnThrTyrProAlaGlnGly 102
                                                                                                                                                                                                                   GluIleAspArgAlaLeuGlyIleProGluLeuValAsnGlnGlyGlnAl 70
                                                                                                                                                                                                                                                                                                                                                                                              o.......ProSerAsnLeuGluGlyGlnSerAspGluArgAlaLeuL
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                                                                                                                                                                            ......CCAAAGCTGCAGAAGCAGGCGCAAAC
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MATHUR, Preete
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0.814
59.877
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alignment_block:
US-09-041-994-2_COPY_1018_1179 x US-60-248-505-604
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Quality:
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NAME/KEY: misc_feature

: LOCATION: (1)...(45333)

: OTHER INFORMATION: n = A,T,C

US-60-248-505-604
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 604, Application US/60248505
GENERAL INFORMATION:
APPLICANT: Beasley, Ellen
TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
FILE REFERENCE: cl000918
CURRENT APPLICATION NUMBER: US/60/248,505
CURRENT FILING DATE: 2000-11-15
NUMBER OF SEQ 1D MOS: 1998
SOFTWARE: FESTENCE for Windows Version 4.0
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LENGTH: 45333
                                                                                                                                                                                                                                                                     20849 TGCTGTTTAGCCAAGTG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20767 TTACAGACTCTTTCAGCACCTACGAAAAATTTAGAACAGCAGGTGAATCA
                                                    20928 AGCACCCGGTTTTACACCTTCAGCCCCAGCAGATAATGCAGCTCCAGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     119 nSerMetMetAsnGlnMetAsnGlnGlnGlyAsnPheProLeuGlnGlyM 136
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88 AspGlnLysAlaGlyLeuTyrGlyGlnThrTyrProAlaGlnGlyProPr 104
                                                                                                                                                                                                                                                                                                                                                                                                                             33 uArgAlaLeuLeuAspGlnLeuHisThrLeuLeuSerAsnThrAspAlaT 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17 LeuAspAspLeuValGlyProProSerAsnLeuGluGlyGlnSerAspGl
                                                                                                                                                          GAAGACACACGTACAGCAGCAGCAGCAGCCAGCAGCAGCAGCAGC
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                                                                                                                                                                                                           nGlnGlyGlnAlaLeuGluProLysGlnAspAlaPheGlnGlyGlnGlu.
                                                                                                                                                                                                                                                                                                                    hrGlyLeuGluGluIleAspArgAlaLeuGlyIleProGluLeu.ValAs 66
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                                                                                                     Ratio:
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0.924
53.797
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Gaps: 8
Percent Identity: 25.949
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APPLICANT: Amy Lasek
TITLE OF INVENTION: GENES EXPRESSED IN LUNG CAI
FILE REFERENCE: PA-0045 P
CURRENT APPLICATION NUMBER: US/60/281,593
CURRENT FILING DATE: 2001-04-04
NUMBER OF SEQ ID NOS: 519
SOFTWARE: PERL PROGRAM
SEQ ID NO 382
LENGTH: 551
TYPE: DNA
ORGANISM: HOMO SapienS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_block:
US-09-041-994-2_COPY_1018_1179 x US-60-281-593-382/rev
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; Sequence 382, Application US/60281593
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_name: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq:US-60-281-593-382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to reverse of: US-60-281-593-382 from: 1 to: 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21075 AGTTTTCACAG.....CAACAGCTACAGTTTCCACAGCAACAGTTGCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21169 GCAGCATGCCTGCAGCAGCAG 21190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
OTHER INFORMATION: Inc:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: unsure LOCATION: 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 etMetAsnGlnMetAsnGlnGlnGlyAsnPheProLeuGlnGlyMetHis 137
                                                                                                                                         105
                                                                                                                                                                                       276
                                                                                                                                                                                                                                                                                 316
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  176
                                                                                                                                                                                                                                                                                                                                                                             364 CCAGAGTTAGTCCAACAAGCTGGGGCAGGGCTGGAGCCCAGGGTCCCN.. 317
                                                                                                                                                                                                                                89 lnLysAlaGlyLeuTyrGlyGlnThrTyrProAlaGlnGlyProPro... 104
                                                                                                                                                                                                                                                                                                                            77 aPheGlnGlyGlnGluAlaAlaValMet...........MetAspG 89
                                                                                                                                                                                                                                                                                                                                                                                                                      62 ProGluLeuValAsnGln...GlyGlnAlaLeuGluProLysGlnAspAl 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAGCAGCAGCAGCAGCTCTCAGCAACCTTACCCCCAGCAG...CCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        uArgMetGlnLeuGlnGlnArg 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCATCCATTTTCACAGCAGCAGCAGCAGCAGCAGCCGCATCCGCATC
AAATCACCTGACTGAGGCACCCAGGCAAGCACCTTGGAGAAGCCAGGGGA 127
                                           nSerMetMetAsnGlnMetAsnGlnGlnGlyAsnPheProLeuGlnGlyM 136
                                                                                           GGGATGAGTGGGGCTCGTCTCAGTGAGCACCACTCAAACAGTTTGGGTCA 177
                                                                                                                                     ...MetGlnGlyGlyPheHisLeuGlnGlyGlnSerProSerPhe...As 119
                                                                                                                                                                                     TGAAGCCTGGCTTAACATGTAAGTCCCACCACAGGGTAGGGCCCACGGAG 227
                                                                                                                                                                                                                                                                                 .....TGGGAATGTGCTCTCTCTCAGGAAGGTGGTTTCTAGACG 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCTCCACAGCAGCTGCATCGCCCTCAGCAGCAGCTCCAGCCCTTTCAGCA 21168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     oMetGlnGlyGlyPheHisLeuGlnGlyGlnSerProSerPheAsnSerM 121
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1.314
56.190
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Gaps: 6
Percent Identity: 30.476
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Sequence 3. Application US/09822687

Sequence 3. Application US/09822687

GENERAL INFORMATION:
APPLICANT: Glucksmann, Maria Alexandra
ITILE OF INVENTION: 31939, A NOVEL HUMAN LEUCINE-RICH REPEAT
TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF
FILE REFERENCE: 10448-038001
CURRENT APPLICATION NUMBER: US/09/822,687
CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: US 60/193,919
PRIOR APPLICATION NUMBER: US 60/193,919
PRIOR APPLICATION NUMBER: US 60/193,919
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 2142
TYPE: DNA
ORGANISM: Homo sapiens
US-09-822-687-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-041-994-2_COPY_1018_1179 x US-09-822-687-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
1946 ACCTGGCCCTGCCCGCCCTGGAGCGAGCCACCTCAACCACCACCACCTAC 1995
                                                                                                                    1896
                                                                                                                                                                                                                                   1846 GAGATCATCAACGTGGAGGACGACCTGCCCGCCGCCTCGGCCGTGTCCGT 1895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1614 CACGGCACC.....CGCCCCGCGCGCTCCTCGCGGCCCCACGGAGAAGGCGT 1657
                                                                                                                                                                                                                                                                                                                                                    1805 AGCACCAGCTCCACAA......GCACCACGGGCCCACGCGCACCGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1708 GACGTCATGAAGACCACCAAAATCATCATCGGCTGCTT...CGTGGCCAT 1754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1658 TCACGGTGCCCATCACGGATGTGACGGAGAACGCCCTCAAGGACCTGGAC 1707
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42 ThrLeuSerAsnThrAspAlaThrGlyLeuGluGluIleAspArgAl 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           145 ProArgThrAsnThr 149
                                                                                                                                                                        92 GlyLeuTyrGlyGln.....
                                                                                                                                                                                                                                                                                                                                                                                                               58 aLeuGlyIleProGluLeuValAsnGlnGlyGlnAlaLeuGluProLysG 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25 erAsnLeuGluGlyGlnSerAspGluArgAlaLeuLeuAspGlnLeuHis 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 HisGlyThrGlnAsnArgProLeuLeuArgAsnSerLeuAspAspLeuVa
                                                                                                                 GGCCGCCGCGGCCGTGGCCAGTGGGGGTGGTGTGGGCGGGGACAGCC 1945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CACGTTCATGGCCGCGGTGATGCTCGTGGCCTTCTACAAGCTGCGCAAGC 1804
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46.316
                                                       .....ThrTyrProAlaGlnGlyProProMetG 106
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seq_documentation_block:
    Sequence 1, Application US/09822687
    Sequence 1, Application US/09822687
    GENERAL INFORMATION:
    APPLICANT: Glucksmann, Maria Alexandra
    TITLE OF INVENTION: 31939, A NOVEL HUMAN LEUCINE-RICH REPEAT
    TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF
    FILE REFERENCE: 10448-038001
    CURRENT APPLICATION NUMBER: US/09/822,687
    CURRENT APPLICATION NUMBER: US/09/822,687
    PRIOR APPLICATION NUMBER: US/09/93,919
    PRIOR FILING DATE: 2001-03-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_block:
US-09-041-994-2_COPY_1018_1179 x US-09-822-687-1
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; NAME/KEY: CDS
; LOCATION: (187)...(2325)
US-09-822-687-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 2493
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                   1894 GACGTCATGAAGACCACCAAAATCATCATCGGCTGCTT...CGTGGCCAT 1940
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                                                                                                                                                                                                1941 CACGTTCATGGCCGCGGTGATGCTCGTGGCCTTCTACAAGCTGCGCAAGC 1990
                                                                                                                                                                                                                                                                                                                                                                                                                           1844 TCACGGTGCCCATCACGGATGTGACGGAGAACGCCCTCAAGGACCTGGAC 1893
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                                                                                                                                                                                                                                42 ThrLeuLeuSerAsnThrAspAlaThrGlyLeuGluGluIleAspArgAl 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 1......GlyProProS 25
75 lnAspAlaPheGlnGlyGlnGluAlaAlaValMetMetAspGlnLysAla 91
                                                                                                                                                                                                                                                                                                                                                                   25 erAsnLeuGluGlyGlnSerAspGluArgAlaLeuLeuAspGlnLeuHis 41
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                                                                                                                                         aLeuGlyIleProGluLeuValAsnGlnGlyGlnAlaLeuGluProLysG 75
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0.881
46.316
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Percent Identity: 24.737
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2032	2032 GAGATCATCAACGTGGAGGACGAGCTGCCCGCCGCCTCGGCCGTGTCCGT 2081	2081	
92	GlyLeuTyrGlyGln	96	
2082	GCCGCCGCGGCCGTGGCCAGTGGGGGTGTGTGGGCGGGGACAGCC	2131	
97		106	
2132	ACCTGGCCCTGCCCCTGGAGCGAGACCACCTCAACCACCACCACTAC	2181	
106	GlnSerProSerPheAsn	122	
2182	2182 GTGGCTGACGCCTTCAAGGC	2210	
123	AsnGlnMetAsnGlnGlyAsnPheProLeuGlnGlyMetHisProAr	139	
2211	CAGCAACCCCAGCGGGGGCTGCGGGGGCAAAGGCCCGC	2251	
139	ProLysGlnLeuArgMetG	156	
2252	CTGGCCTCAACTCCACGAACCTCTGCT	2282	
156			
2283	CTTCAAGAGCGGCTCCAA 2300		

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/cgn2_6/ptodata/1/ina/5B_COMB.ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OM of: US-09-041-994-2_COPY_613_752 to:
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/cgn2_6/ptodata/1/ina/5B_COMB
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/cgn2_6/ptodata/1/ina/5B_COMB
/cgn2_6/ptodata/1/ina/6A_COMB
                                                                                                                                                                                                                                                                                                                                                                                                                                       /cgn/
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-(a-/cg12_1/USPTO_spco1/US09041994/runat_30042001_165631_19495/app_query.fasta_1.1940
-DB-Issued_Patents_NA -(PRMT-fastap -SUFFIX-p2n.rni
-GAPOP-12.000 -GAPEXT=4.000 -MINMATCH-0.100 -LOOPCL-0.000
-LOOPEXT=0.000 -GAPEXT=4.000 -MINMATCH-0.100 -XGAPOP-10.000
-XGAPEXT=0.000 -GAPOP-4.500 -GAPEXT=7.000 -YGAPOP-10.000
-XGAPEXT=0.500 -DELOP-6.000 -DELEXT=7.000 -YGAPOP-10.000
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-MATRIX-blosum62 -TRANS-human40.cdi -LIST=45 -DOCALIGN=200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Results were produced by the GenCore software, Copyright (c) 1993-2000 Compugen Ltd.
                                       1:US-08-864-038A-2 -
1:US-08-864-038A-4 -
1:US-08-072-610-1 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Issued_Patents_NA:*
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cgn2_6/ptodata/1/ina/5A_COMB.seq:US-08-194-088B-15-
/cgn2_6/ptodata/1/ina/5B_COMB.seq:US-08-194-087-15-
/cgn2_6/ptodata/1/ina/FBTUS_COMB.seq:PCT-US93-04648-15-
/cgn2_6/ptodata/1/ina/5B_COMB.seq:US-08-861-664-13+
/cgn2_6/ptodata/1/ina/5B_COMB.seq:US-08-396-001-13+
US-07-667-276A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 215-875-8394
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Weiser & Associates
STREET: 230 S. Fifteenth Street,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/0: FILING DATE: 11-MAR-1991 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 2017 base pairs
                                                                                                  FEATURE:
                                                                                                                                                   FEATURE:
                                                                                                                                                                                                FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                   ANTI-SENSE: NO
                                                                                                                                                                                                                                               HYPOTHETICAL:
                                                                                                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
               OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                 STRAIN: S288C
                                                                                                                                                                                  ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 215-875-8394
                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Weiser, Gerard J. REGISTRATION NUMBER: 19, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                  LOCATION:
                                                                                                                                                                                                                                                                                     TOPOLOGY:
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                                                                 LOCATION:
                                                                               NAME/KEY:
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                                                                                                                                                                                                                                                                                                                 nucleic acid
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                                                                                                                CDS
484..1725
                                                                                                                                                                                                                                                                                 unknown
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                                                                               misc_feature
                                                                                                                                                                                  Saccharomyces cerevisiae
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                                                                                                                                                                                                                 internal
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                                                                                                                                                                                                                                                                  DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRESS-INDUCED PROTEINS, GENES CODING THEREFOR, TRANSFORMED CELLS OF ORGANISMS, METHODS APPLICATIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US/07667276A
          /note* "Base #1 of Sequence No. 5470971 3 corresponds to base -483 of the sequence Figure 11 of the application"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US/07/667,276A
                                                                                                                                                                                                                                                                                                                                                                                                                                                 19,763
                                                                                                                                                                                                                                                                                                                                                                                                                                     377.5351P
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alignment_block: US-09-041-994-2_COPY_613_752 x US-07-667-276A-3

alignment_scores: Quality:

Percent Similarity:

Ratio:

86.00 1.132 63.333

Length: Gaps: Percent Identity:

120 2 24.167

Align seg 1/1

to: US-07-667-276A-3

from: 1

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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence 1, Application US/08209747
Patent No. 5733771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                         INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                      TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Lewis, Randolph V.
APPLICANT: Colgin, Mark
TITLE OF INVENTION: CDNAS Enc
TITLE OF INVENTION: Silk Prot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  104 CysGlyAspGlyAsnValValLysGlnGluGlnLeuSerProLysLysLy 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  713 AAGCTGAAACCAAGAAGGAAGAATCCAAGGATTCCTCTTCCTCTTCCTCT 762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        602 CATCTTCATCTGAATCTGAATCTGAGTCTGAGTCTGAATCTGAATCTTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        555 AGCT...AAGGCCGTCTCCTCCTCCTCCGAATCTTCATCCTCATCTT 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         505 AAAGGTAACAAGAAGGAAGTTAAGGCTTCCAAACAAGCCAAAGAAGAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       763 GACTCTTCTTCCGACGAAGAAGAAGAAGAAGAAAAGAAGAAACCAAGAA 812
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54 GlyValSerSerThrSerAsnMetHisGlySerLeuLeuGlnGluLysHi 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20 gGlyHisSerSerLeuThrAsnSerProLeuAspSerSerCysLysGluS 37
                                                                                                                                             NAME: Murphy Jr., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Birch, Stewart, Kolasch & Birch STREET: P.O. Box 747 CITY: Falls Church
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 LysGlyH1sLysLeuLeuGlnLeuLeuThrCysSerSerAspAspAr
                                                                                                  TELEPHONE:
                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/209,747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
     LENGTH:
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2793 base pairs
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                                                                                                  703-205-8000
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                                                                                                                                                  1447-104P
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; NAME/KEY: CDS; LOCATION: 183..2675; OTHER INFORMATION: /producto "N. clavipes minor; OTHER INFORMATION: ampullate silk protein" US-08-209-747-1
                                                                                                                                                                                                                                                                                                                                                                                   seq_name: /cgn2_6/ptodata/1/ina/5A_COMB.seq:US-08-458-298-1
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Quality:
                                                                                                                                                                                                                                                                                                                                                seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/08458298 Patent No. 5756677
                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: do TOPOLOGY: linear MOLECULE TYPE: cDN HYPOTHETICAL: NO ORIGINAL SOURCE: ORGANISM: Nephil
  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                      TITLE OF INVENTION:
                                                                                                                                                                                                                                              APPLICANT: Lewis, Rando
APPLICANT: Colgin, Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       710
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                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          611 ACCAGCTCCAGCACCAGCACCTCTACCGTAACCACCAGCGCCTCCGGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      760 GCTCCAGCACCAGCACCTCTACCGTAACCGCCAGCACCTCCTGCTCCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   860 TCCTGCTCCAGCAGCAGCAGCAGCCGCACCAGCTCCTGCTCCGGCACCGT 811
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                                                                                                    ADDRESSEE: Birch, St. STREET: P.O. Box 747 CITY: Falls Church
                                         COUNTRY: USA
ZIP: 22040-3487
                                                                                 STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    GlyAsnSerProAlaGluValAlaLysIleThrAlaGlnAlaThrGlyLy 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCAGCAGCAGCCG.CACCAGCTCCTGCTCCGGCACCATATCCGCCT 662
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                                                                                                                                                                                                                                                                                                                                                                                                                             CTGCTCCAGCAGCTGCAGCAGCACCAGCTCCGGCTCCGGCACCATA 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGTCCACCATATCCAGCACCACCGGCGCGCCTGCACCTGCCCCAGCAGCCGC 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SerSerThrSerAsnMetHisGlySerLeuLeuGln......
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Virginia
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                                                                                                                                                                                                                                                                Lewis, Randolph V.
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E: minor ampullate
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Floppy disk
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1.176
61.207
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                                                                                                                                                                                                      cDNAs Encoding Minor Ampullate Spider Silk Proteins
                                                                                                                                         Stewart,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps: 4
Percent Identity: 31.897
                                                                                                                                           Kolasch & Birch
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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-458-298-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to reverse of: US-08-458-298-1 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-041-994-2_COPY_613_752 x US-08-458-298-1/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 703-205-8050 INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HYPOTHETICAL: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 08/209,747
FILING DATE: 14-MAR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                            611 ACCAGCTCCAGCACCAGCACCTCTACCGTAACCACCAGCGCCTCCGGCTC
                                                                                                                                                                                             661 TGTCCACCATATCCAGCACCACCGGCGCCTGCACCTGCCCCAGCAGCCGC
                                                                                                                                                                                                                                                                                                                                                                                           760 GCTCCAGCACCACCTCTACCGTAACCGCCAGCACCTCCTGCTCCTGC 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             810 ACCCACCTTGACCACCGTAGCCTCCAGCTCCAGCACCCGCAGCGGCTCCT 761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            860 TCCTGCTCCAGCAGCAGCAGCAGCCGCACCAGCTCCTGCTCCGGCACCGT 811
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 703-205-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
561 CTGCTCCAGCAGCTGCAGCAGCACCAGCTCCGGCTCCGGCACCATA 516
                                           96 sAspThrSerSerIle.....ThrSerCysGlyAspGlyAsnVal 109
                                                                                                                                                                                                                                                                                                                                        56 SerSerThrSerAsnMetHisGlySerLeuLeuGln......
                                                                                                                                          80 GlyAsnSerProAlaGluValAlaLysIleThrAlaGlnAlaThrGlyLy 96
                                                                                                                                                                                                                                                                                                                                                                                                                                         39 alSerValThrSerProSerGlyValSerSerSerThrSerGlyGlyVal 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14 ThrCysSerSerAspAspArgGlyHisSerSer.......... 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: 183..2675
OTHER INFORMATION: /product= "N. clavipes minor OTHER INFORMATION: ampullate silk protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Nephila clavipes TISSUE TYPE: minor ampullate gland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: doub
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1447-104P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Murphy Jr., Gerald M. REGISTRATION NUMBER: 28,977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/0 FILING DATE: 02-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE:
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                                                                                                                                                                                                                          ......GluLysHisArgIleLeuHisLysLeuLeuGln.Asn 79
                                                                                                                                                                                                                                                                                          ACCAGCAGCAGCCG.CACCAGCTCCTGCTCCGGCACCATATCCGCCT 662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .....LeuThrAsnSerProLeuAspSerSerCysLysGluSerSerV 39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ratio:
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1.176
61.207
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alignment_block:
US-09-041-994-2_COPY_613_752 x US-08-320-559-29
                                                                                                                                      alignment_scores:
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                                                                                                                                                                                          US-08-320-559-29
 Align seg 1/1 to: US-08-320-559-29
                                                                                  Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 29, Application US/08320559 Patent No. 5633135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF
                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 3376 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/888,830
FILING DATE: 27-MAY-92
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APPLICATION NUMBER: US,
FILING DATE: 30-OCT-92
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: WORDPERFECT 5.1 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Croce, Carlo APPLICANT: Canaani, Eli TITLE OF INVENTION: Diag
                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
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NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF
                                                                                                                                                                                                         NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: 11-DE
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: One Liberty
CITY: Philadelphia
                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 33,229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE:
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                                                                                                                      Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19103
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196..1902
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ne Liberty Place - 46th Floor
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                                                                                                                                                                                                                                                           DNA (genomic)
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                                                                                  82.00
1.000
48.235
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Detection and Treatment of Acute Leukemias
Resulting from Chromosome Abnormalities in the
All-1 Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PC-DOS
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                                                                                  Gaps:
Percent Identity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                      TJU-0855
from: 1 to: 3376
                                                                                                                      Length:
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24.706
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7 LysLysLeuLeuGlnLeu

LeuThrCysSe

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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 29, Application US/08545860D Patent No. 6040140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Croce, Carlo
APPLICANT: Croce, Eli
TITLE OF INVENTION: Diagnostics, Therapeutics and Methods
TITLE OF INVENTION: For Detection and Treatment of Acute Leukemias
TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the
NUMBER OF SEQUENCES: 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1092 AAAGAGTAGC 1101
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                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         992 ATAGTAACTTACTCACCATCACCAGTGGACAAGATAAGAAGGCTCCTAGT 1041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   942 TAAGATGGCCTTCAAGGAACCTAAACCCATGTCAAAAGAGCCAAAACCAG 991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                742 AGCAGCAGCAGCAGCAGTAGTACCAGTTTTTCAAAGCCTCACAAATT 791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           692 GCAGTAGCAGCAGCAGCAGCAGCAGCAGCAGCAGTAGCAGCAGCAGT 741
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   792 AATGAAGGAGCACAAGGAAAAACCTTCTAAAGACTCCAGAGAACATAAAA 841
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                                                                                                                                                                                                                                                         STATE: F
                                            APPLICATION NUMBER: US/08/545,860D FILING DATE: 07-MAR-1996
                                                                                                                                                                                                                                                                                                     STREET: One Liberty Place, 46th floor CITY: Philadelphia
                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Woodcock, Washl
ADDRESSEE: No. 6040140ris
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .....SerAsnMetHisGlyS 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .....ValValLysGlnGluGlnLeuSerProLysLysLysGl 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..... 108
APPLICATION DATA:
                                                                                                                                                                                                                                        19103
                                                                                                                                                                                                                                                                             Pennsylvania
                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .....AsnSerProAlaGluValAlaLysIleThrAl 91
                                                                                                                                                                                                                                                                                                                                                                          Woodcock, Washburn, Kurtz, Mackiewitz
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US-09-041-994-2_COPY_613_752 x US-08-545-860D-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-545-860D-29
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REGISTRATION NUMBER: 33,229
REFERENCE,DOCKET NUMBER: TJU-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEPAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 29:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                   592 AGAAAGTTGCTGAAGGCAGGAGGGGACCCTAATAGGAGTATTCATACCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 07/805,093
FILING DATE: 11-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: DeLuca Esq., Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/888,839
EILING DATE: 27-MAY-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 30-OCT-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/320,559
FILING DATE: 11-OCT-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 19-OCT-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/US92/10930 FILING DATE: 09-DEC-1992 PRIOR APPLICATION DATA:
                                                                                                                                                                                                             692 GCAGTAGCAGCAGCAGCAGCAGCAGCAGCAGCAGTAGCAGCAGCAGT 741
                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: 15
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                      792 AATGAAGGAGCACAAGGAAAAACCTTCTAAAGACTCCAGAGAACATAAAA 841
                                                                                                                                                          50 SerThrSerGlyGlyValSerSerThr.....
                                                                                                                                                                                                                                                       33 erCysLysGluSerSerValSerValThrSerProSerGlyValSerSer 49
                                                                                                                                                                                                                                                                                                                                16 rSerAspAspArgGlyHisSerSerLeuThrAsnSerProLeuAspSerS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE: 22-APF
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                                                                                                              AGCAGCAGCAGCAGCAGTAGTACCAGTTTTTCAAAGCCTCACAAATT 79:
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Ratio:
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196..1902
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19-OCT-1994
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1.000
48.235
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                                                          .....SerAsnMetHisGlyS 64
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691 ω 641

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alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 29, Application PC/TUS9404496 GENERAL INFORMATION:
                                                                                                                                                                                                                                                 TELEFAX: (215) 568-343 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1092 AAAGAGTAGC 1101
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                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: TJ
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: DeLuca Esq., Mark
REGISTRATION NUMBER: 33,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 uAsnAsnAla 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                892 TCTAAGAAACCCAAAGAAAATAAACCACTGAAAGAAGAGAAAATAGTTCC 94;
                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Resulting from Chromosome Abnormalities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NPPLICANT: Canaani, Eli
TITLE OF INVENTION: Diagnostics, Therapeutics and Methods
TITLE OF INVENTION: for Detection and Treatment of Acute Leukemias
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91 aGlnAlaThrGlyLysAspThrSer..........
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                                                                                    NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: One Liberty Place, 46th floor CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 19103
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                                                                                                                                                                                                                                                                                            (215) 568-3439
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                                                                                    196..1902
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seq_documentation_block:
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US-09-041-994-2_COPY_613_752 x PCT-US94-04496-29
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                                                                                                                                                                                                                                                                  Patent No.
                                                                                                                                                                                                                                                                                 Sequence 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1042
                                                                                         TITLE OF INVENTION: TITLE OF INVENTION:
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                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    892
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                   STREET:
                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                             AAAGAGTAGC
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                                                                                                                                                                                                                                            INFORMATION:
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Ratio:
New York
                                                                                                                                                                                                                                                                               Application US/08728323A
                 E: Cooper & Dunham LLP
1185 Avenue of the Americas
                                                                                                                                                                Chang, Yuan
Bohenzky, Roy A.
Russo, James J.
Edelman, Isidore S.
                                                                                                                                            Edelman, Isidore
Moore, Patrick S.
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1.000
48.235
                                                                    Immediate Early Protein From Kaposi's Sarcoma-Associated Herpesvirus, DNA Encoding Same And Uses Thereof
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ZIP: 10036 COMPUTER READABLE FORM:

MEDIUM TYPE:

Floppy disk

COUNTRY:

?Y: U.S.A. 10036

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seq_documentation_block:
; Sequence 20, Application US/08770379
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    Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; NAME/KEY:
; LOCATION:
US-08-728-323A-1
                                                              seq_name: /cgn2_6/ptodata/1/ina/5B_COMB.seq:US-08-770-379-20
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TELEPHONE: 212-291-0525
TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
TENGTH: 3489 base pairs
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Percent Similarity:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US.
FILING DATE:
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                           67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34 ysLysGluSerSerValSerValThrSerProSerGlyValSerSerSer 50
                                                                                                                                                                                                                                                                                                                                                                                                            51 ThrSerGlyGlyValSerSerThrSerAsnMetH1sGlySerLeuLeuGl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 LeuGluSerLysGlyHisLysLysLeuLeuGlnLeuLeuThrCysSerSe 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                          IleThrSerCysGlyAspGlyAsn 108
                                                                                                       TCTGTCTCCTGCTCCTCATCA 990
                                                                                                                                                                                              CCTCGTCATCCTCGTCATCCTCCTCGTCATCCTCGTCCTCCTCA 1014
                                                                                                                                                                                                                                    laGluValAlaLysIleThrAlaGlnAlaThrGlyLysAspThrSerSer 100
                                                                                                                                                                                                                                                                                                                         nGluLysHisArgIleLeuHisLysLeuLeuGlnAsnGlyAsnSerProA 84
                                                                                                                                                                                                                                                                                 .....TCGTCATCCT 1064
                                                                                                                                                                                                                                                                                                                                                                    TCCTCCTCGTCATCCTCGTCATCCTCGTCATCCTCC..... 1074
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alignment_block:
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GENERAL INFORM
APPLICANT:
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INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 5234
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
                                                                                                                                                                                                                                                                                                                                                                  20732 TIGICCTCCTCCTCGTCATCCTCCTCGTCCTCATTGTCCTCATCATCGTC 20781
                                                                                                                                                                                 20832 CCTCCTCCTCGTCATCCTCCTCGTCATCCTCGTCATCCTCCTCGTCA 20881
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ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Bohenzky, Roy A.
APPLICANT: Russo, James J.
APPLICANT: Edelman, Isidore S.
APPLICANT: Moore, Patrick S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: POLYPEPTIDES FROM KAPOSI'S SARCOMA-ASSOCIATED TITLE OF INVENTION: HERPESVIRUS, DNA ENCODING SAME AND USES THEREOF NUMBER OF SEQUENCES: 20
                                                                                51 ThrSerGlyGlyValSerSerThrSerAsnMetH1sGlySerLeuLeuGl 67
:::|||::::: |||||:::|||::: ::|||
882 TCCTCCTCGTCATCCTCCTCGTCATCCTCCTCCTCCC....... 20
                                                                                                                                                                                                                           34 ysLysGluSerSerValSerValThrSerProSerGlyValSerSerSer 50
                                                                                                                                                                                                                                                                                                                   17 rAspAspArgGlyHisSerSerLeuThrAsnSerProLeuAspSerSerC 34
                                                                                                                                                                                                                                                                                                                                                                                          1 LeuGluSerLysGlyHisLysLysLeuLeuGlnLeuLeuThrCysSerSe 17
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: New York
STATE: New York
COUNTRY: U.S.A.
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
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                                        nGluLysHisArgIleLeuHisLysLeuLeuGlnAsnGlyAsnSerProA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION:
CANT: Chang, Yuan
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Ratio:
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Percent Identity:
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.....TCGTCATCCT 20933
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alignment_block:
US-09-041-994-2_COPY_613_752 x US-08-757-669A-20
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                                                                                                                                                            Align seg 1/1 to: US-08-757-669A-20
                                                                                                                                                                                                                                                              Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Atenc No. GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL TONGO
APPLICANT: Chang, Yuan
ADPLICANT: Bohenzky, Roy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (212) 391-05; INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20984 TCTGTCTCCTGCTCCTCATCA 21007
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ATTORNEY AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS TITLE OF INVENTION: SEQUENCES AND USES THEREOF
                                 17 rAspAspArgGlyHisSerSerLeuThrAsnSerProLeuAspSerSerC 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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                                                                                                                1 LeuGluSerLysGlyHisLysLysLeuLeuGlnLeuLeuThrCysSerSe 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/757,669A FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
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                                                                               TTGTCCTCCTCGTCATCCTCCTCGTCCTCATTGTCCTCATCATCGTC
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6183751
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) 391-0525
NO: 20:
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Percent Identity:
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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: WordPerfect 6.1/Windows
SEQ ID NO 3
LENGTH: 397
TYPE: DNA
ORGANISM: human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Dong Kyu JIN
APPLICANT: Dong Kyu JIN
TITLE OF INVENTION: Diagnostic Method and Kit for Neurope
TITLE OF INVENTION: USing Trinucleotide Repeats Sequence
FILE REFERENCE: 1942/36
CURRENT APPLICATION NUMBER: US/09/253,691
CURRENT FILING DATE: 1999-02-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/09253691 Patent No. 6124100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EARLIER APPLICATION NUMBER: KR 98-6,278 EARLIER FILING DATE: 1996-02-26
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                                        sLysLeuLeuGlnAsnGlyAsnSerProAlaGluValAlaLysIleThrA 91
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                                                                                                                                           ThrSerAsnMetHisGlySerLeuLeuGlnGluLysHisArgIleLeuHi
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                                                                                        AGCAGCAGCAGCAGCAGCAGCAGCAGCAGC.......
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Ratio:
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.AGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCA 315
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1.162
69.388
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                                                                                                                                           74
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seq_documentation_block:
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Percent Similarity:
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Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (212)953-7733
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-:
FILING DATE: 15-July-1996
ATTORNEY/AGENT INFORMATION:
NAME: C. Bruce Hamburg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Diskette, 3.50 inch, 1.44
COMPUTER: IBM Compatible
OPERATING SYSTEM: Microsoft Windows 95
SOFTWARE: Word Perfect 6.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
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                                           421 CTCCTGCGCCTGCTCCAGCACCAGCACCAGCACCACCTCCGGCACCACCA 372
                                                                                                                                471 ACCTCCGAGACCTCCGCCCAATCCAAGTCCGAGTCCAGCACCTGCTCCTG 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
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                                                                                                                                                                              16
    49
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CELL TYPE: mantle epithel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/864,038A FILING DATE: May 28, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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erSerThrSerGlyGlyValSerSerThrSerAsnMet..HisGlySerL
                                                                                  rSerCysLysGluSerSerValSerValThrSerProSerGlyValSerS 49
                                                                                                                                                                         SerSerAspAspArgGlyHisSerSerLeuThrAsnSerProLeuAspSe 32
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5. 6001592
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1.539
60.714
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CONTAINING SAID CDNA, HOST CELLS TRANSFORMED WITH SAID
VECTOR, POLYPEPTIDE PRODUCED THEREBY, METHOD OF PRODUCING
SAID POLYPEPTIDE, DNA ENCODING SAID POLYPEPTIDE AND ANTIBODY
TO SAID POLYPEPTIDE
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seq_name: /cgn2_6/ptodata/1/1na/6A_COMB.seq:US-08-864-038A-2
                                                      alignment_scores:
                                                                                                            US-08-864-038A-2
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 Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                          TELEFAX: (212)953-7733
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: JP 8-184459
FILING DATE: 15-ULLY-1996
ATTORNEY/AGENT INFORMATION:
NAME: C. Bruce Hamburg
REGISTRATION NUMBER: 22,389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/864,038A FILING DATE: May 28, 1997 PRIOR APPLICATION DATA:
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Word Perfect
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskett
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TITLE OF INVENTION:
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                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                   MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                271 CACCGCCGCCGCGCGTCCGCCGTCGGCTCCTCCAGCACCGCCAGCTCCC 222
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                                                                                                                                                                                   ORGANISM: Pinctada fucata CELL TYPE: mantle epithel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
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                                                                                                                             LOCATION: from 1 to 3 IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                               LENGTH:
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                                     Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SYSTEM: Microsoft Windows Word Perfect 6.1
                                                                                                                                                                                                                                                         linear
                                                                                                                                              from 1 to 3331
                                                                                                                                                                                 mantle epithelial cell
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78.50
1.539
60.714
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 Gaps:
Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3.50 inch, 1.44 MB storage
                                                                                                                             (by experiment)
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29.762
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alignment_block:
US-09-041-994-2_COPY_613_752 x US-08-864-038A-2/rev
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                                                                                        INFORMATION FOR SEQ ID NO:
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                         APPLICATION NUMBER: JP 8-184459
FILING DATE: 15-7011y-1996
ATTORNEY/AGENT INFORMATION:
NAME: C. Bruce Hamburg
REGISTRATION NUMBER: 22,389
REFERENCE/DOCKET NUMBER: F-5610
                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Word Perfect
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.
COMPUTER: IBM Compatible
OPERATING SYSTEM: Microsc
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                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     320 CACCGCCGCCGCCGCCGTCCGCCGTCCGCTCCAGCACCGCCAGCTCCC 271
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                                                                                                                                                     TELECOMMUNICATION INFORMATION:
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CITY: Tsu-city
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                                                                                                                                TELEPHONE:
STRANDEDNESS:
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                                      ENGTH:
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                     nucleic acid
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                                                                                                        (212)953-7733
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                                                                                                                                  (212)986-2340
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seq_name: /cgn2_6/ptodata/1/ina/5A_COMB.seq:US-08-072-610-1
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   Quality:
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                                                                                                                                                                                                                                                                                                                                                                               Patent No.
                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1,
                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:

NAME/KEY: CDS

LOCATION: from 50 to

IDENTIFICATION METHOD:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                          APPLICANT: Barnwell, TITLE OF INVENTION: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   320 CACCGCCGCCGCGCGTCGCCGTCGGCTCCAGCACCACCGCCAGCTCCC
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                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 270 C 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         470 CTCCTGCGCCTGCTCCAGCACCAGCACCAGCACCTCCGGCACCACCA 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: cDNA to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83 o 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49 erSerThrSerGlyGlyValSerSerThrSerAsnMet..HisGlySerL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16 SerSerAspAspArgGlyHisSerSerLeuThrAsnSerProLeuAspSe 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM:
CELL TYPE:
                                APPLICATION NUMBER: FILING DATE: 19930
                                                                                                                                                                     COUNTRY: USA
ZIP: 10022-7513
                                                                                                                                                                                                       STATE:
                                                                                                                                                                                                                                         STREET:
                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     euLeuGlnGluLysHisArgIleLeuHis.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCATTCATCATCGTCATCGCTGTCGTCATCATAGTCATATTCCCCAATCTC
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                                                                                                                                                                                                                         New York
                                                                                                                                                                                                                                                                                                                                                                                 5532133
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                                                                                                                                                                                                       New York
                                                                                                                                                                                                                                         805 Third
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                        US/08/072,610
19930602
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1.539
60.714
                                                                                                                                                                                                                                                                                                        Plasmodium vivax Blood Stage Antigens, Monoclonal Antibodies, and Diagnostic Assays
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                                                                                                                                                                                                                                                                                                                                             John
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cell
                                                                                   Version #1.25
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: 29.762
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NAME: Gogoris, Adda REGISTRATION NUMBER:

29,714

5986/07686

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seq_documentation_block:
    Sequence 1, Application US/08719822B
    Patent No. 5874527
    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                              seq_name: /cgn2_6/ptodata/1/ina/5B_COMB.seq:US-08-719-822B-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-072-610-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (212)753-623:
TELEX: 236687
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                             2163 GTACCTCTTCCACTTCTACTTCTGCAGGT 2132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2213 TACCTCTTCCACTTCTTCTACTTCTGCGGGTACCTCTTCTACTTCTTCTG 2164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2277 GTACCTCTTCCACTTCTTCTGGTACCTCTTCCACTTCTTCTGGTACCTCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2227 TCC.....ACTTCTTGG
                                                                                                                                             APPLICANT: Barnwell, John TITLE OF INVENTION: Plasme NUMBER OF SEQUENCES: 4
                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby and Darby
STREET: 805 Third Ave.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORIGINAL SOURCE:
ORGANISM: Plasmodium vivax
IMMEDIATE SOURCE:
CLONE: PVMB3.3.1
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HYPOTHETICAL: NO
ANTI-SENSE: NO
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LENGTH: 337 base pairs
TYPE: NUCLEIC ACID
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)527-7700
TELEFAX: (212)753-6237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47 alSerSerThrSerGlyGlyValSerSerThrSerAsnMetHisGly 63
                                                                                                                                                                                                                                                                                                                                                                                                         97 spThrSerSerIleThrSerCysGlyAspGly 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80 yAsnSerProAlaGluValAlaLysIleThrAlaGlnAlaThrGlyLysA 97
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                    COUNTRY:
                                                            CITY: New York
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XY: USA
10022-7513
                                       New York
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1.377
60.638
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                                                                                                                                                                       Plasmodium vivax Blood Stage Antigens
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alignment_block:
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US-08-719-822B-1
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TELEFAX: (212)753-6237
TELEX: 236687
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                          2227
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HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
2163 GTACCTCTTCCACTTCTTCTACTTCTGCAGGT
                                                                                                                                                                                     2213 TACCTCTTCCACTTCTTCTACTTCTGCGGGTACCTCTTCTACTTCTTCTG 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2277 GTACCTCTTCCACTTCTTCTGGTACCTCTTCCACTTCTTCTGGTACCTCT 2228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2368 ACCTCTTCTACTACCGCTGGTACTTCTACTTCTACTACCGCTGGTAC 2319
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CLONE: PVMB3.3.1
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LENGTH: 3337 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                80 yAsnSerProAlaGluValAlaLysIleThrAlaGlnAlaThrGlyLysA 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 SerLeuLeuGlnGluLysHisArgIleLeuHlsLysLeuLeuGlnAsnGl 80
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                                                                                97 spThrSerSerIleThrSerCysGlyAspGly 107
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TYPE: nucleic acid
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REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 5986/17686US2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 0 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: UPPER DESCRIPTION NUMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                TCC.....ACTTCTTCGG
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1.377
60.638
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Percent Identity: 30.851
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of: US-09-041-994-2_COPY_613_752 to: Pending_Patents_NA_Main:*

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Database: Pending_Patents_NA_Main:*
Database sequences: 13168883
Database length: -1691701393
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search information block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Command line parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Search time (sec): 4537.790000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -Q-/Ggn2_1/USPTO_Spool/US09041994/runat_30042001_165632_19506/app_query.fasta_1.1940
-DB=Pending_Patents_NA_Main -QFWT=fastap -SUFFIX=p2n.rnpm
-GAPOP=12.000 -GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000
-LOOPEXT=0.000 -QGAPOP=4.500 -GAPEXT=0.050 -YGAPOP=10.000
-YGAPEXT=0.500 -FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000
-YGAPEXT=0.500 -DELOP=6.000 -DELEXT=7.000 -YGAPOP=10.000
-YGAPEXT=0.500 -DELOP=6.000 -DELEXT=7.000 -YGAPOP=10.000
-YGAPEXT=0.500 -DELOP=6.000 -DELEXT=7.000 -YGAPOP=10.000
-YGAPEXT=0.500 -TRANS=human40.cdi -LICST=45 -DOCALIGN=200
-THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTEMT=pfs -NORM=ext -MINLEN=0 -MAXLEN=200000000
-USER-USO9041994_@CGN1_1_8354 -NCPU=6 -ICPU=3 -LONGIOG -NO_XLPXY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WAIT -THREADS=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MODEL=frame+_p2n.model -DEV=xlp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Results were produced by the GenCore software, Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-041-994-2_COPY_613_752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /ptodata/1/pna/US090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           _COMB.seq:US-09-041-994-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ! Documentation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        version
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9.9e-51 4859
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                                                                                                                                                           6156
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6835
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                               1972
                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
34 ysLysGluSerSerValSerValThrSerProSerGlyValSerSerSer
                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
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seq_documentation_block:
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/cgn2_6/ptodata/1/pna/US097A_COMB.seq:US-09-716-972-4617
/cgn2_6/ptodata/1/pna/US097B_COMB.seq:US-09-721-599-6496
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/cgn2_6/ptodata/1/pna/US097B_COMB.seq:US-09-726-788-7097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: /cgn2_6/ptodata/1/pna/US090_COMB.seq:US-09-041-994-1
                                                                                                                                                                                                                                         Ratio:
Percent Similarity:
                                                                                                                                              Align seg 1/1 to: US-09-041-994-1 from: 1 to:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 617-742-4214
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Chen, J. APPLICANT: Li, Hui TITLE OF INVENTION: TITLE OF INVENTION:
                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-227-7400
TELEFAX: 617-742-4214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0.
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION: NAME: Liepmann, W. Hugo
                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                 17 rAspAspArgGlyHisSerSerLeuThrAsnSerProLeuAspSerSerC
                                                                                      1 LeuGluSerLysGlyHisLysLysLeuLeuGlnLeuThcCysSerSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 4496 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Liepmann, W. Hugo REGISTRATION NUMBER: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/041,994 FILING DATE:
TGATGACCGGGGTCATTCCTCCTTGACCAACTCCCCCCTAGATTCAAGTT
                                                                                                                                                                                                                                                                                Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Boston
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28 State Street
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86..4338
                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                           5.021
100.000
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                                                                                                                                                                                                                                                                                703.00
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Percent Identity:
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22222
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2072 ACATCTGGAGGAGTATCCTCTACATCCAATATGCATGGGTCACTGTTACA 2121

ThrSerGlyGlyValSerSerThrSerAsnMetHisGlySerLeuLeuGl

51

67 nGluLysHisArgIleLeuHisLysLeuLeuGlnAsnGlyAsnSerProA 84

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alignment_block:
US-09-041-994-2_COPY_613_752 x US-09-513-066-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; NAME/KEY: CDS
; LOCATION: (86)..(4330)
US-09-513-066-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: UMG-026CP
CURRENT APPLICATION NUMBER: US/09/513,066
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: USSN 09/041,994
PRIOR FILING DATE: 1998-03-13
PRIOR APPLICATION NUMBER: USSN 60/073,674
PRIOR FILING DATE: 1998-02-04
NUMBER OF SEQ ID NOS: 37
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                Quality: 703.00
Ratio: 5.021
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: /cgn2_6/ptodata/1/pna/US095A_COMB.seq:US-09-513-066-1
                                                                                                                                                                                                                                                                      Align seg 1/1 to: US-09-513-066-1 from: 1 to: 4496
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Chen, J. Don
APPLICANT: Leo, Christopher
APPLICANT: Li, Hui
TITLE OF INVENTION: NOVEL USES FOR THE RAC3 TRANSCRIPTIONAL COACTIVATOR OF
TITLE OF INVENTION: STEROID NUCLEAR RECEPTORS
                                                            1972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 4496
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2322 ATCCTAGTGATGCACTCTCT 2341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2272 TAAGAAGAAGGAGAATAATGCACTTCTTAGATACCTGCTGGACAGGGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2122 AGAGAAGCACCGGATTTTGCACAAGTTGCTGCAGAATGGGAATTCACCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              117 oLysLysGluAsnAsnAlaLeuLeuArgTyrLeuLeuAspArgAspA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       101 IleThrSerCysGlyAspGlyAsnValValLysGlnGlnGlnLeuSerPr 117
                                                                                  17 rAspAspArgGlyHisSerSerLeuThrAsnSerProLeuAspSerSerC 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84 laGluValAlaLysIleThrAlaGlnAlaThrGlyLysAspThrSerSer 100
34 ysLysGluSerSerValSerValThrSerProSerGlyValSerSerSer 50
                                                                                                                                                                                            LeuGluSerLysGlyHisLysLysLeuLeuGlnLeuLeuThrCysSerSe 17
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                                                       TGATGACCGGGGTCATTCCTCCTTGACCAACTCCCCCCTAGATTCAAGTT
                                                                                                                                                                ATAACTTCTTGTGGGGACGGAAATGTTGTCAAGCAGGAGCAGCTAAGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTGAGGTAGCCAAGATTACTGCACAAGCCACTGGGAAAGACACCAGCAGT 2221
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Percent Identity: 100.000
                                                       2021
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1,
                                                                                                                                                                                         TELEFAX: 973-683-4117
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                            CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Walsh, andrea C.
REGISTRATION UNMBER: 97.88
REFERENCE/DOCKET NUMBER: 9724
TELECOMMUNICATION INFORMATION:
TELEPHONE: 973.683-2169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2272 TAAGAAGAAGGAGAATAATGCACTTCTTAGATACCTGCTGGACAGGGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2222 ATAACTTCTTGTGGGGACGGAAATGTTGTCAAGCAGGAGCAGCTAAGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Suen, Chen-Shian
APPLICANT: Frail, Donald E.
APPLICANT: Lyttle, Richard C.
TITLE OF INVENTION: Cloning and Expression of a Nuclear
TITLE OF INVENTION: Receptor Coactivator Proteins and Uses Thereof
NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: US/60/068,51
                    ORIGINAL SOURCE:
                                                           HYPOTHET ICAL:
                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                134 spProSerAspAlaLeuSer 140
                                           ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          101 IleThrSerCysGlyAspGlyAsnValValLysGlnGluGlnLeuSerPr 117
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ORGANISM:
                                                                                                           STRANDEDNESS:
TOPOLOGY: lir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: UZIP: 07054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Parsippany
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: American Home Products Corporation
                                                                                                                                                                         LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  oLysLysCysGluAsnAsnAlaLeuLeuArgTyrLeuLeuAspArgAspA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nGluLysHisArgIleLeuHisLysLeuLeuGlnAsnGlyAsnSerProA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTGAGGTAGCCAAGATTACTGCACAAGCCACTGGGAAAGACACCAGCAGT
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                                                                                                                                                  nucleic acid
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                                                                                                                                                                           4789 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      One Campus Drive
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Homo sapiens
                                                                                                           linear
                                                                                       CDNA
                                                                                                                              single
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; NAME/KEY: ; LOCATION: US-60-068-511-1

CDS 185..4750

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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity: 100.000
                                                                              NUMBER OF SEQ ID NOS: 47
SEQ ID NO 1
LENGTH: 6754
TYPE: DNA
                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                           Sequence 1, Application US/09440612
NAME/KEY: CDS
LOCATION: (184)..(4422)
-09-440-612-1
                                                                                                                                                                           APPLICANT: C. Frank Bennett
APPLICANT: Lex M. Cowsert
TITLE OF INVENTION: ANTISENSE MODULATION OF
FILE REFERENCE: RTS-0042
                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/440,612 CURRENT FILING DATE: 1999-11-15
                                                                ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2321
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                                                 FEATURE:
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Ratio:
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alignment_scores:
    Quality:
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; Sequence 3, Application US/09440612A
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US-09-041-994-2_COPY_613_752 x US-09-440-612-1
                                                                                                      ; NAME/KEY: CDS
; LOCATION: (184)..(4422)
US-09-440-612-3
                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: /cgn2_6/ptodata/1/pna/US094_COMB.seq:US-09-440-612-3
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                                                                                                                                                                                        FILE REFERENCE: RTS-0042
CURRENT APPLICATION NUMBER: US/09/440,612A
CURRENT FILING DATE: 1999-11-15
NUMBER OF SEQ ID NOS: 49
SEQ ID NO 3
LENCTH: 6754
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                  APPLICANT: C. Frank Be APPLICANT: Lex M. Cowsert
                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
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Percent Similarity:

Percent

Identity:

99.286

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alignment_block:
                                                                                     alignment_scores:
Quality:
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; NAME/KEY: CDS
; LOCATION: (201)..(4463)
US-09-125-635-1
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us-09-041-994-2_COPY_613_752 x us-09-440-612-3
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US-09-041-994-2_COPY_613_752 x US-09-125-635-1
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: THE UNITED STATES OF AMERICA represented by THE SE
TITLE OF INVENTION: AIB1, A novel steriod receptor co-activator
FILE REFERENCE: 49944
CURRENT APPLICATION NUMBER: US/09/125,635
CURRENT FILING DATE: 1998-08-21
PRIOR APPLICATION NUMBER: 60/049,728
PRIOR APPLICATION NUMBER: 60/049,728
PRIOR FILING DATE: 1997-06-17
NUMBER OF SEC ID NOS: 12
COPTEMBRE OF SEC ID NOS: 12
                                                                                                                                                                                                                                                                                  SOFTWARE:
SEQ ID NO 1
                                                                                                                                                                                                                           LENGTH: 6835
TYPE: DNA
ORGANISM: Homo:
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                                               Similarity:
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                                                                 Ratio:
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                                                 100.000
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                                                 Identity:
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                                                  99.286
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Sequence 3962, Application US/09359922

GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
APPLICANT: Hyseq, Inc.
ITITLE OF INVENTION: NOVEL CONTIGS OBTAINED FROM VARIOUS CDN
ITITLE OF INVENTION: LIBRARIES
FILE REFERENCE: 20411-752CON1
CURRENT APPLICATION NUMBER: US/09/359,922
CURRENT FILING DATE: 1999-07-22
EARLIER APPLICATION NUMBER: US 09/205,155
EARLIER FILING DATE: 1998-12-03
NUMBER OF SEQ ID NOS: 13203
SOFTMARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3962
LENGTH: 6855
TYPE: DNA
                                                                                                                                                                              ; FEATURE:

NAME/KEY: misc_feature

LOCATION: (1)...(6855)

OTHER INFORMATION: n =

US-09-359-922-3962
                                                                                                            alignment_scores:
    Quality:
                                                 alignment_block:
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                             US-09-041-994-2_COPY_613_752 x US-09-359-922-3962
 Align seg 1/1
                                                                              Percent Similarity:
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2087

TGATGACCGGGGTCATTCCTCCTTGACCAACTCCCCCCTAGATTCAAGTT rAspAspArgGlyHisSerSerLeuThrAsnSerProLeuAspSerSerC 34

2136

2086 17

17

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APPLICANT: LESTHOWILZ, Dena
APPLICANT: Liu, Jin
TITLE OF INVENTION: NOVEL CONTIGS OBTAINED FROM VARIOUS cDNA
TITLE OF INVENTION: LIBRARIES
FILE REFERENCE: 20411-752CON1
CURRENT APPLICATION NUMBER: US/09/359,922A
CURRENT FILING DATE: 1999-07-22
EARLIER APPLICATION NUMBER: US 09/205,155
EARLIER APPLICATION NUMBER: US 09/34,341
EARLIER FILING DATE: 1998-12-03
EARLIER FILING DATE: 1998-02-13
NUMBER OF SEQ ID NOS: 13203
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3962
alignment_block:
us-09-041-994-2_copy_613_752 x us-09-359-922-3962
                                                                                      alignment_scores:
Quality:
                                                                                                                                                            ; NAME/KEY: misc_feature
; LOCATION: (1)...(6855)
; OTHER INFORMATION: n =
US-09-359-922-3962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: /cgn2_6/ptodata/1/pna/US093_COMB.seq:US-09-359-922-3962
                                                   Quality: 700.00
Ratio: 5.000
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3962,
                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                               LENGTH: 6855
TYPE: DNA
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^N· n = A,T,C (
                                                       Length: 140
Gaps: 0
Percent Identity: 99.286
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alignment_block:
US-09-041-994-2_COPY_613_752 x US-60-209-009-198
                                                                                                                                    ; NAME/KEY: unsure
; LOCATION: 3941-3993, 5899-5939, 6951
; OTHER INFORMATION: a, t, c, g, or other
US-60-209-009-198
                                                                                                                                                                                                                                                                                                                                                                                                                               seq_documentation_block:
; Sequence 198, Application US/60209009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: /cgn2_6/ptodata/1/pna/US6020_COMB.seq:US-60-209-009-198
                                               Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: US-09-359-922-3962 from:
                                                                                                                                                                                                                                                                  FILE REFERENCE: PA-0027 P
CURRENT APPLICATION NUMBER: US/60/209,009
CURRENT FILING DATE: 2000-06-01
NUMBER OF SEQ ID NOS: 501
SOFTWARE: PERL Program
SEQ ID NO 198
LENGTH: 7116
                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Faris, I
APPLICANT: Pearson
                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Pearson, Cecelia I. TITLE OF INVENTION: GENES
                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                      NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: 1094199.1
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                                                              Quality:
Ratio:
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                                               700.00
5.000
100.000
                                             Length: 140
Gaps: 0
Percent Identity: 99.286
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; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 1094199.1
; NAME/KEY: unsure
; LOCATION: 3941-3993, 5899-5939, 6951
; OTHER INFORMATION: a, t, c, g, or other
US-60-213-360-7991
   alignment_block:
                                                                                          alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: /cgn2_6/ptodata/1/pna/US6021_COMB.seq:US-60-213-360-7991
                                   Quality: 700.00
Ratio: 5.000
Percent Similarity: 100.000
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CURRENT APPLICATION NUMBER: US/60/213,360
CURRENT FILLING DATE: 2000-06-21
NUMBER OF SEQ ID NOS: 8347
SOFTWARE: PERL Program
SEQ ID NO 7991
LENGTH: 7116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Morris,
                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Lal, Preeti
APPLICANT: Diep, Dinh
APPLICANT: Diep, Dinh
TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide Polymor
TITLE OF INVENTION: Identified Thereby
TITLE OF INVENTION: GX-0014 P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 7991,
                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                          TYPE: DNA
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Lal, Preeti
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                                     Percent Identity:
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                                                                                                                                                                                                                                           APPLICANT: HOLLMAN, Douglas A.
FITTLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND
FILE REFERENCE: 1600.1186-001
CURRENT APPLICATION NUMBER: US/09/652,123
CURRENT FILING DATE: 2000-08-30
PRIOR APPLICATION NUMBER: 60/151,135
PRIOR APPLICATION NUMBER: 60/151,135
PRIOR FILING DATE: 1999-08-30
NUMBER OF SEQ ID NOS: 9796
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8947
LENGTH: 7888
TYPE: DNA
TODANISM: Homo Sapiens
                                                                   alignment_block:
US-09-041-994-2_COPY_613_752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_documentation_block:
   Sequence 8947, Application US/09652123
   GENERAL INFORMATION:
                                                                                                                                                                                                                                    ; ORGANISM: Homo sapiens US-09-652-123-8947
                                                                                                                                                                               alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_name: /cgn2_6/ptodata/1/pna/US096C_COMB.seq:US-09-652-123-8947
                                 Align seg 1/1
                                                                                                                      Quality: 700.00
Ratio: 5.000
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TAAGAAGAAGAATAATGCACTTCTTAGATACCTGCTGGACAGGGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTAAAGAATCTTCTGTTAGTGTCACCAGCCCCTCTGGAGTCTCCTCCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nGluLysHisArgIleLeuHisLysLeuLeuGlnAsnGlyAsnSerProA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to: US-60-213-360-7991 from: 1 to:
                                   to: US-09-652-123-8947
                                                                     x US-09-652-123-8947
                                                                                                                        Gaps:
Percent Identity:
                                   from: 1 to: 7888
                                                                                                                        140
0
99.286
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2436

2386

2336

2286 84 2236 2186

2136

2086 34

17

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alignment_block:
US-09-041-994-2_COPY_613_752 x US-09-652-127-9831
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Quality: 700.00
Ratio: 5.000
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                   ; TYPE: DNA; ORGANISM: Homo sapiens US-09-652-127-9831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: /cgn2_6/ptodata/1/pna/US096C_COMB.seq:US-09-652-127-9831
                                                                                                        Align seg 1/1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 9831, Application US/09652127 GENERAL INFORMATION: APPLICANT: Shyjan, Andrew W.
                                                                                                                                                                                                                                                                                                            SEQ ID NO 9831
LENGTH: 7888
                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Shyjan, Andrew W.
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600,1118-001
CURRENT APPLICATION NUMBER: US/09/652,127
CURRENT FILING DATE: 2000-08-30
PRIOR APPLICATION NUMBER: 60/151,134
                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 19
NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2298
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17 rAspAspArgGlyHisSerSerLeuThrAsnSerProLeuAspSerSerC
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                                                             LeuGluSerLysGlyHisLysLysLeuLeuGlnLeuLeuThrCysSerSe 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nGluLysHisArgIleLeuHisLysLeuLeuGlnAsnGlyAsnSerProA
                                            laGluValAlaLysIleThrAlaGlnAlaThrGlyLysAspThrSerSer 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTGAGGTAGCCAAGATTACTGCAGAAGCCACTGGGAAAGACACCAGCAGT
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                                                                                                                                                                                                                                                                                                                                           FastSEQ for Windows Version
                                                                                                      US-09-652-127-9831 from: 1
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Identity:
                                                                                                      to:
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seq_documentation_block:

Sequence 11050, Application US/09652355

GENERAL INCOMNATION:

APPLICANT: Shyjan, Andrew W.

TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USE

TITLE OF INVENTION: THEREFOR

FILE REFERENCE: 1600.1192-001

CURRENT APPLICATION NUMBER: US/09/652,355

CURRENT FILING DATE: 2000-08-30

PRIOR APPLICATION NUMBER: 60/151,136

PRIOR APPLICATION NUMBER: 300
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                                                                                                                                                                                                                                                 alignment_block:
US-09-041-994-2_COPY_613_752 x
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Quality:
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                                                                                                                                                                                                                   Align seg 1/1 to:
                                                                                                                                                                                                                                                                                                        Ratio:
Percent Similarity:
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SOFTWARE: FastSEQ for
SEQ ID NO 11058
LENGTH: 7888
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2098 TGATGACCGGGGTCATTCCTCCTTGACCAACTCCCCCCTAGATTCAAGTT
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                                                                                      17 rAspAspArgGlyHisSerSerLeuThrAsnSerProLeuAspSerSerC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FastSEQ for Windows
                                                                                                                                                                                                                 US-09-652-355-11058 from: 1 to:
                                                                                                                                                                                                                                                                                                        700.00
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Percent Identity:
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seq_documentation_block:
Sequence 1028, Application US/09663693
GENERAL INFORMATION:
APPLICANT: Gearing, David P.
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.1195-001
CURRENT APPLICATION NUMBER: US/09/663,693
CURRENT APPLICATION NUMBER: 05/09/663,693
CURRENT FILING DATE: 1909-09-21
PRIOR APPLICATION NUMBER: 60/154,986
PRIOR FILING DATE: 1999-09-21
NUMBER OF SEQ ID NOS: 1340
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1028
LENGTH: 7888
TYPE: DNA
CORGANISM: Homo sapiens
US-09-663-693-1028
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Quality:
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Ratio: 5.000
Percent Similarity: 100.000
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                                                           LeuGluSerLysGlyHisLysLysLeuLeuGlnLeuLeuThrCysSerSe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ThrSerGlyGlyValSerSerThrSerAsnMetHisGlySerLeuLeuGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IleThrSerCysGlyAspGlyAsnValValLysGlnGluGlnLeuSerPr 117
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                                                                                                                                                                                                                                                                                                                                      Percent Identity: 99.286
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; SEQ ID NO 5135
; LENGTH: 7888
; TYPE: DNA
; ORGANISM: Homo saplens
US-09-698-014-5135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Gearing, David P.
APPLICANT: Holtzman, Douglas A.
APPLICANT: Kingsbury, Gillian A.
APPLICANT: Kingsbury, Gillian A.
APPLICANT: Kingsbury, Gillian A.
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREFOR
TILE REFERENCE: 1600.2014-001
CURRENT APPLICATION NUMBER: US/09/698,014
CURRENT FILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: 60/162,363
PRIOR APPLICATION NUMBER: 60/162,363
PRIOR FILING DATE: 1999-10-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality:
Ratio:
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Percent Identity: 99.286
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May 1,

9:18

of: US-09-041-994-2_COPY_613_752 to:

Pending_Patents_NA_New:*

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Command line parameters:

Results were produced by the GenCore software, Copyright (c) 1993-2000 Compugen Ltd.

version

72.00 72.00 72.00

105.15 0 103.27 0 103.07

243.12 249.49 309

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Search time (sec): 114.180000
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Database sequences: 201016
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-Q-/cgn2_1/USPTO_spc01/US09041994/runat_30042001_165632_19523/app_query.fasta_1.1940
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-GAPDP-12.000 -GAPEXT-4.000 -MINMATCH-0.100 -LOOPCL-0.000
-LOOPEXT-0.000 -GAPEXT-4.000 -MINMATCH-0.100 -KAPOP-10.000
-XGAPEXT-0.500 -GAPEXT-0.000 -GAPEXT-7.000 -YGAPOP-10.000
-YGAPEXT-0.500 -DELOP-6.000 -DELEXT-7.000 -YGAPOP-10.000
-YGAPEXT-0.500 -DELOP-6.000 -DELEXT-7.000 -YGAPOP-10.000
-YGAPEXT-0.500 -DELOP-6.000 -DELEXT-7.000 -YGAPOP-10.000
-YGAPEXT-0.500 -THR_MAX-100 -THR_MIN-0 - ALIGN-15 -MODE-LOCAL
-OUTFMT-pfs -NORM-ext -MINLEN-0 -MAXLEN-200000000
-USEP-US09041994_@CGN1_1_175 -NCPU-6 -ICPU-3 -LONGLOG -NO_XLPXY
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                      134
                      spProSerAspAlaLeuSer 140
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Sequence 1, Application US/09196296B
GENERAL INFORMATION:
APPLICANT: Suen, Chen-Shian
APPLICANT: Frail, Donald E.
APPLICANT: Lyttle, Richard C.
APPLICANT: Lyttle, Richard C.
TITLE OF INVENTION: Cloning and Expression of a Nuclear
TITLE OF INVENTION: Receptor Coactivator Proteins and Uses
FILE REFERENCE: 0630/01376
CURRENT APPLICATION NUMBER: US/09/196,296B
CURRENT FILING DATE: 1998-11-19
NUMBER OF SEQ ID NOS: 3
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US-09-041-994-2_COPY_613_752 x US-09-196-296B-1
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Quality:
Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:US-09-663-561-6 + /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:US-09-663-561-33 + /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:US-09-663-561-33 + /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:US-08-956-1710-63 + /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq:PCT-US01-09718-136 -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 1 LENGTH: 4789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo
                                                                                                                                                                                                                                                                                             67 nGluLysHisArgIleLeuHisLysLeuLeuGlnAsnGlyAsnSerProA
                                                                                                                                                                                                                                                                                                                                                                                                                                                2071 TGATGACCGGGGTCATTCCTCCTTGACCAACTCCCCCCTAGATTCAAGTT
                                                                                            101 IleThrSerCysGlyAspGlyAspValValLysGlnGlnGlnLeuSerPr 117
                                                                                                                                              17 rAspAspArgGlyHisSerSerLeuThrAsnSerProLeuAspSerSerC
ATAACTTCTTGTGGGGACGGAAATGTTGTCAAGCAGGAGCAGCTAAGTCC
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seq_documentation_block:
; Sequence 12210, Applic
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US-09-041-994-2_COPY_613_752 x US-09-335-032-12207/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-335-032-12207
                                                                                   seq_name: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:US-09-335-032-12210
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Quality:
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    Sequence 12207, Applic
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SOFTWARE: FastSEO for Windows Version 4.0
SEO ID NO 12207
LENGTH: 1531974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Velculescu, Victor
APPLICANT: Vogelstein, Bert
APPLICANT: Winzler, Kenneth
TITLE OF INVENTION: Characterization of the Yeast
TITLE OF INVENTION: Transcriptome
FILE REFERENCE: 01107.78572
CURRENT APPLICATION NUMBER: US/09/335,032
CURRENT FILING DATE: 1999-06-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59771 CAGTGTGAAAACCACATCTCCTACCAATACTCATGAGCATTCTAAAGCGA 59722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59821 GGTCATTCCAGTGCTACCACTTCCCCTGTCACCTCACACATGGTCATGC 59772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/035,917
PRIOR FILING DATE: 1997-01-23
PRIOR APPLICATION NUMBER: US 09/012,031
PRIOR FILING DATE: 1998-01-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59671 ACTACCCACCCTGTTAGCCATGGTCACTCTGGTTCAAGCACTGGTCCTAA 59622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59721 ATACTGGTCCATCAGCCACTGCAACTACACATGGACATATCAACGTCAAA 59672
                                                                                                                                                                                                                                                                                                                                                                                                                                       101
                                                                                                                                                                                                    134 pProSerAsp 137
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                                                                                                                                            CAACTCAGAT 59495
                                                                                                                                                                                                                                                                                                                   LysLysCluAsnAsnAlaLeuLeuArgTyrLeuLeuAspArgAspAs 134
                                                                                                                                                                                                                                                                                                                                                                              TTACTCAT...GGACATACAAGTGTT.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATCCACCGCTGCTGCACAGGATCATTCCAGTACTAAAACTAACCCTTCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GluLysHisArgIleLeuHisLysLeuLeuGlnAsnGlyAsnSerProAl 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                erGlyGlyValSerSerThrSerAsnMetHisGlySerLeu...LeuGln 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rSerValSerValThrSerProSerGlyVal.....SerSerSerThrS 52
                                                                                                                                                                                                                                                                                                                                                                                                                                 leThrSerCysGlyAspGlyAsnValValLysGlnGluGlnLeuSerPro 117
                                                                                                                                                                                                                                                             .....AAAGATAACTCCTCAGCTACGAAGGGTTATTCGAACACTGATTC 59505
Application US/09335032
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58.333
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Percent Identity: 26.667
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alignment_block:
US-09-041-994-2_COPY_613_752 x US-09-335-032-12210
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Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: US-09-335-032-12210 from: 1 to: 1090936
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SEQ ID NO 12210
LENGTH: 1090936
                                                              161599 GATAGACGCTTGTCTATATCCTCGCTGAATCCATCTAATGCATTATCA 161646
                                                                                                                                                                                   161549 CATCATCTTCCAGTGGAGGTAGTGATGGGTCTAGGCGACCATCTTTGGTG 161598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          161364 AGAGAAGAATCGGTTGAAGTTAATTCATTGGCAGACGACGTTGCTCAA, 161412
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                                                                                                                                                                                                                                                                                                                                                                                                                                  161449
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                                                                                                                                                                                                                                                                                                          161499 TCAACAGTATTTTCAAAATCAAGGAGAAAATCCGAGGTTACTGAGGGCCA 161548
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APPLICANT: Vogelstein, Bert
APPLICANT: Kinzler, Kenneth
TITLE OF INVENTION: Characterization of the
TITLE OF INVENTION: Transcriptome
FILE REFERENCE: 01107.78572
CURRENT APPLICATION NUMBER: US/09/335,032
CURRENT FILING DATE: 1999-06-16
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PRIOR FILING DATE: 1997-01-23
PRIOR APPLICATION NUMBER: US 09/012,031
PRIOR FILING DATE: 1998-01-22
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                                                                                                                 131 AspArgAsp.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47 alSerSerSerThrSerGlyGlyValSerSerThrSerAsn.....Met 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 HisGlySerLeuLeuGlnGluLys......HisArgIleLe 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16 SerSerAspAspArgGlyHisSerSerLeuThrAsnSerPro.....Le 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73 uHisLysLeuLeuGlnAsnGlyAsnSerProAla...GluValAlaLysI 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30 uAspSerSerCysLysGluSerSerValSerValThrSerProSerGlyV 47
                                                                                                                                                                                                                                                                                                                                                                                                                           TCAACTCAAAATCAGAACGTCTTATTGAATGAGCAATTCTCTCCAAACAA 161498
                                                                                                                                                                                                                                                                                                                                                                   sLys....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .....GCAGGATTCAATCCAAATCCTATTAAGCACCCAACT 161448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        leThrAlaGlnAlaThrGlyLysAspThrSerSerIle.....Thr 102
/cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:US-09-335-032-12210
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0.941
56.024
                                                                                                                    ...........AspProSerAspAlaLeuSer 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps: 10 Percent Identity: 27.711
                                                                                                                                                                                                                                        .....TyrLeuLeu 130
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seq_documentation_block:

GENERAL INFORMATION:

Sequence 12210, Application US/09335032

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seq_documentation_block:
    Sequence 9282, Application PC/TUS0101339
    GENERAL INFORMATION:
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US-09-041-994-2_COPY_613_752 x US-09-335-032-12210/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-335-032-12210
                                                                                                                            seq_name: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq:PCT-US01-01339-9282
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                                                                                                                                                                                                                                                                                       442056 ATTGCATATTCACCATATAATGATGATGGCTCTTGTAAGTCTGCAGACGC 442007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    442102
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TITLE OF INVENTION: Characterization of the
TITLE OF INVENTION: Transcriptome
FILE REFERENCE: 01107.78572
CURRENT APPLICATION NUMBER: US/09/335,032
CURRENT FILING DATE: 1999-06-16
APPLICANT: Human Genome Sciences, Inc., et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/035,917
PRIOR FILING DATE: 1997-01-23
PRIOR APPLICATION NUMBER: US 09/012,031
PRIOR FILING DATE: 1998-01-22
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                                                                                                                                                                                                                                      138
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                                                                                                                                                                                  TGTCTCT 442000
                                                                                                                                                                                                                                   aLeuSer 140
                                                                                                                                                                                                                                                                                                                                     LeuArgTyrLeuLeuAspArgAspAspProSer.....AspAl 138
                                                                                                                                                                                                                                                                                                                                                                                                                                         alValLysGlnGluGlnLeuSerProLysLysLysGluAsnAsnAlaLeu 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGGTTCCTCTAGTAGCAGCGCTGCTATAACTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nAlaThrGlyLysAspThrSerSerIleThrSerCysGlyAspGlyAsnV 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LeuLeuGlnAsnGlyAsnSerProAlaGluValAlaLysIleThrAlaG1 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     erAsnMetHisGlySerLeuLeuGlnGluLysHisArgIleLeuHisLys 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTCTTCTTCTACTTCCTCTACTTCTTCTTCTACTTCTTCCTCTACTT 442161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rSerProSerGlyValSerSerSerThrSerGlyGlyValSerSerThrS 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .....TCTACTTCATCCACACAGGAAACAGCCGCTACCACCTCTGA 442103
                                                                                                                                                                                                                                                                                                                                                                                           .....TCTCCAAAG.....
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1.426
51.261
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seq_documentation_block:
; Sequence 12214, Applic:
; GENERAL INFORMATION:
; APPLICANT: Velculescu
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US-09-041-994-2_COPY_613_752 x PCT-US01-01339-9282/rev
                                                                                                                                 seq_name: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:US-09-335-032-12214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_scores:
Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 9282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: PCT/US01/01339
CURRENT FILING DATE: 2001-03-17
NUMBER OF SEQ ID NOS: 10231
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Nucleic Acids, Proteins, FILE REFERENCE: PC006PCT
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TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2099 ACGCCAGCCAAGTAGCTGGGACCTCAGCCTCCCAAGTAGCTGGGACCTCA 2050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2149 CTGCCTCCCAGGCTCAAGCCATGCTCCCAAGTAGCTGGGACTACAGGCAC 2100
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LOCATION: (4456)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1952 GTCATGAACTCACGAGCTCAAGCAATCTGCACACCTCGGTTCCCAAAGTG 1903
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                                                                                                                                                                                                                                       rLeuLeuAspArgAspAspPro 135
                                                                                                                                                                                                                                                                                                                                                   GlnGluGlnLeuSerProLysLysLysGluAsnAsnAlaLeuLeuArgTy 128
                                                                                                                                                                                                                                                                                                                                                                                                        AACAAGCTTCCCAGATGGTTCAAATGCACACTTCAGTTTGGTAACTACTG 180:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTGGGATTACAGGCATGAGCCACTGCGCCTGGCTGAGAACCTGCATTTTT 1853
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                                                                                                                                                                                    TCTCCTGTCCAAGAATTCCCCA 1731
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                                                  Application US/09335032
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55.063
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Velculescu,

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alignment_block:
US-09-041-994-2_COPY_613_752 x US-09-335-032-12214/rev
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                                                                                                                                                                                                                                                               seq_name: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:US-09-335-032-12212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_scores:
Quality:
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                                                                                                                                                          Sequence 12212, Application US/09335032 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 1997-01-23
PRIOR APPLICATION NUMBER: US 09/012,031
PRIOR FILING DATE: 1998-01-22
NUMBER OF SEQ ID NOS: 12219
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12214
                      APPLICANT: Velculescu, Victor
APPLICANT: Vogelstein, Bert
APPLICANT: Kinzler, Kenneth
TITLE OF INVENTION: Characterization of the Yeast
TITLE OF INVENTION: Transcriptome
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TITLE OF INVENTION: Characterization of the Yeast
TITLE OF INVENTION: Transcriptome
FILE REFERENCE: 01107.78572
CURRENT APPLICATION NUMBER: US/09/335,032
CURRENT FILING DATE: 1999-06-16
PRIOR APPLICATION NUMBER: US 60/035,917
TITLE OF INVENT
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                                                                                                                                                                                                                                                                                                                                                                                                                          TCAGAAGATGAAACCAAGAAAAGAGCAAGAGAATCAGACAACGAAGATGC 613110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .GluGlnLeuSerProLysLysLysGluAsnAsnAlaLeuLeuArgTyrL 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ysAspThrSerSerIleThrSerCysGlyAspGlyAsnValValLysGln 112
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ON: Transcriptome 01107.78572
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Percent Identity:
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CURRENT APPLICATION NUMBER: US/09/335,032
CURRENT FILING DATE: 1999-06-16
PRIOR APPLICATION NUMBER: US 60/035,917
PRIOR FILING DATE: 1997-01-23
PRIOR APPLICATION NUMBER: US 09/012,031
PRIOR FILING DATE: 1998-01-22
NUMBER OF SEQ ID NOS: 12219
SOFTWARE: FBSTSEQ for Windows Version 4.0
SEQ ID NO 12212
LENGTH: 439885
TYPE: DNA
                                                                      APPLICANT: Velculescu, Victor
APPLICANT: Vogelstein, Bert
APPLICANT: Kinzler, Kenneth
TITLE OF INVENTION: Characterization of the Yeast
TITLE OF INVENTION: Transcriptome
FILE REFERENCE: 01107.7852;
CURRENT APPLICATION UNMBER: US/09/335,032
CURRENT FILING DATE: 1999-06-16
PRIOR APPLICATION NUMBER: US 60/035,917
PRIOR FILING DATE: 1997-01-23
PRIOR FILING DATE: 1997-01-23
PRIOR FILING DATE: 1998-01-22
PRIOR FILING DATE: 1998-01-22
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Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                           Sequence 12218, Application US/09335032 GENERAL INFORMATION:
NUMBER OF SEQ ID NOS: 12219
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25362 GGCAGCCAATCAGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23 SerSerLeuThrAsnSerProLeuAspSerSerCysLysGluSerSerVa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ratio:
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Percent Identity: 28.571
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; LENGTH: 1091282 TYPE: DNA ; ORGANISM: Saccharomyces cerevisiae US-09-335-032-12218

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CURRENT APPLICATION NUMBER: US/09/335,032
CURRENT FILING DATE: 1999-06-16
PRIOR APPLICATION NUMBER: US 60/035,917
PRIOR FILING DATE: 1997-01-23
PRIOR APPLICATION NUMBER: US 09/012,031
PRIOR FILING DATE: 1998-01-22
NUMBER OF SEQ ID NOS: 12219
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 12212
EENCTH: 439885
                                                    alignment_scores:
                                                                                                                                ; ORGANISM: Saccharomyces cerevisiae US-09-335-032-12212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: US-09-335-032-12218 from: 1 to: 1091282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-041-994-2_COPY_613_752 x US-09-335-032-12218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 12212, Application US/09335032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                427959 ATCATCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCATCAT 428008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   428159 CGACTATCTTGCCAACAATCTCATTTGCATCCATCATCCCACTTAACCCG 428208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      428109 CTCTTCTTCCTTTCCCGCAGAAACATCGGGATAACCACCTAGTTTGA 428158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        428059 CCACCAGTATCGTTCTTATTATCATCCTCCTCATCGTTATCTTCATC 428108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                427909 TCGTCGTCGTCGTCGTCATCATCGTCGTCATCATCGTCGTCATCATC 427958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 428209 ATGT 428212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Velculescu, Victor
APPLICANT: Vogelstein, Bert
APPLICANT: Kinzler, Kenneth
TITLE OF INVENTION: Characterization of the Yeast
TITLE OF INVENTION: Transcriptome
FILE REFERENCE: 01107.78572
                                                                                                                                                                                    TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     103 rCys 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88 LysIleThrAlaGlnAlaThrGlyLysAspThrSerSer...IleThrSe 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75 ysLeuLeu.........GlnAsnGlyAsnSerProAlaGluValAla 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49 erSerThrSerGlyGlyValSerSerThrSerAsnMetHisGlySer... 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32 rSerCysLysGluSerSerValSerValThrSerProSerGlyValSerS 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16 SerSerAspAspArgGlyHisSerSerLeuThrAsnSerProLeuAspSe 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .....LeuLeuGlnGluLys.HisArgIleLeuHisL 75
  Quality:
Ratio:
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1.297
62.745
  82.00
1.079
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Length:
Gaps:
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111
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alignment_block:
US-09-041-994-2_COPY_613_752 x US-09-335-032-12208
                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Saccharomyces cerevisiae US-09-335-032-12208
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US-09-041-994-2_COPY_613_752 x US-09-335-032-12212
                                                                                                                                                                                                                                                                                                              alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:US-09-335-032-12208
                                                                                     Align seg 1/1 to: US-09-335-032-12208 from: 1 to: 574860
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                                                                                                                                                                                                                            Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 12208, Application US/09335032
GENERAL INFORMATION:
APPLICANT: Velculescu, Victor
APPLICANT: Vogelstein, Bert
APPLICANT: Kinzler, Kenneth
TITLE OF INVENTION: Characterization of the
TITLE OF INVENTION: Transcriptome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID.NO 12208
LENGTH: 574860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              334423 AATAGCTCCTCCTCTGCTACCTCCAAGAACGCT 334455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              334373 CTGCAGCTTCCTCTTCTGCAAAGGCCTCCTCTTCTGCAGAAAAATCTACT 334422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       334273 TCTTCTGCTTCTGAAGCTGCTAAGTCTTCTAGCTCTGCCAAGTCTTCTGG 334322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 09/012,031 PRIOR FILING DATE: 1998-01-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/035,917 PRIOR FILING DATE: 1997-01-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/335,032 CURRENT FILING DATE: 1999-06-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: 01107.78572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 114 GlnLeuSerProLysLysLysGluAsnAsnAla 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47 alSerSerThrSerGlyGlyValSerSerThrSerAsnMetHisGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97 spThrSerSerIleThrSerCysGlyAspGlyAsnValValLysGlnGlu 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80 yAsnSerProAlaGluValAlaLysIleThrAlaGlnAlaThrGlyLysA 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64
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16 SerSerAspAspArgGlyHisSerSerLeuThrAsnSerProLeuAspSe
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                                                                                                                                                                                                                                                                                 Quality:
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62.105
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Percent Identity:
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seq_documentation_block:
    Sequence 480, Application US/08956171C
    GENERAL INFORMATION:
;
US-08-956-171C-480
                                                                                                                                 ATTORNEY AGENT INFORMATION:

NAME: HOOVEY, KEDLEY K.

REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PB248P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 610-5790
TELEPAX: (301) 309-6439
INFORMATION FOR SEQ ID NO: 480:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79230 CATCATCTTCTTCTTCTTCTTCTTCTTCTTCTTGCTACTAAGAACGGA 79279
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                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171C
FILING DATE: 20-Oct-1997
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCGCCTCCAGCAGTACAAGCTCAATGAGCGGTAAT 79384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rSerCysLysGluSerSer.....ValSerValThrSerProSerGlyV 47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTCAACTAAGAAGAGTAGTAAGACTAGTTCCACCGCTTCATCATCATCAT 79229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Charles Kunsch
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                                                                  LENGTH: 6309 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Rockville
STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Human Genome SciensTREET: 9410 Key West Avenue
                    DESCRIPTION: SEQ ID NO: 480:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20850
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genome Sciences, Inc
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Ratio:
Percent Similarity:
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                                        COUNTRY:
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seq_documentation_block:
; Sequence 220, Application US/08956171C
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         124 AlaLeuLeuArgTyrLeuLeuAspArg......AspAsp 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         454 ...GAAGTCTTAAAACAAGATCAAAACAAACCATTACCAGTCGAACACCAA 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    420 TGCAAGTAAATTAGAACGTGGTAAACGTACTGTT.........
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            329 AGAAAGTTGCTGGTACGTTACGTCTTGACTTAGCGTCATACAGAGAACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 229 TTCTTACAATCTGATTTATTCTTCTCAGGTGTAAGACCAGCGATTAATGC 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            179 TTTCAGCTTATGTACCAACAAACGTTATTTCAATTACAGATGGACAAATC 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       132 CGGTTCAATTACTGCATTACCAATTATCGAAACA...CAAGCTGGTGATA 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90 rAlaGlnAlaThrGlyLysAspThrSerSerIleThrSerCysGlyAspG 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74 HisLysLeuLeuGlnAsnGlyAsnSerProAlaGluValAlaLysIleTh 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39 alserValThrSerProSerGlyValSerSerSerThrSerGlyGlyVal 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82 CATAGTAGATTATTAGAAAGAGCAGCAAAATTAAACGATGACTTAGGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22 sSerSerLeuThrAsnSerProLeuAspSerSerCysLysGluSerSerV 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 HisLysLysLeuLeuGlnLeuLeuThrCysSerSerAspAspArgGlyHi 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGGACAATCTGTATCTCGTGTTGGTGGATCTGCACAAATTAAAGCAATGA 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lyAsnValValLysGlnGluGlnLeuSerProLysLysLysGluAsnAsn 123
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
                                                                                                                                                                                                                                                                                    Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ....SerSerThrSerAsnMetH1sGlySer.........
                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Charles Kunsch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:US-08-956-171C-220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .....LeuLeuGlnGluLysHisArgIleLeu 73
                                                                                                                                             CITY: Rockville
STATE: Maryland
                                                                                                                                                                                                    STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to: US-08-956-171C-480
                                                                                                                                                                                                                                                                                                                                                                                               Craig A. Rosen
                                                                                                                                                                                                                                                                                                                                                                                                                            Patrick S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78.50
0.946
50.610
                                                                                                                      USA
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Gaps: 6
Percent Identity: 22.561
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OPERATING SYSTEM: MSDOS version 6.2 SOFTWARE: ASCII Text

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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to reverse of: US-08-956-171C-220 from: 1 to: 13059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-041-994-2_COPY_613_752 x US-08-956-171C-220/rev
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11958 GAGCACATCCGATTCGACAAGCACATCCGAATCACTGAGTACATCTATGT 11909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12008 ACATCAATTAGTGACTCAGAATCAGTGTCAACAAGCACATCAACGTCATT 11959
11608 TTGGTTTAGGTTTAATGAAGAGAAAGAAAAAGAAAGATGAAAAT.....
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                                                                                                                                                                                                                                                                                                                          11758 CGAGCACGAGTGAATCTCAGTCTACATTAAGTGCAACATCTGAAGTGACT 11709
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                                                                                                                                                                                                                                                                    103 SerCysGly.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42 hrSerProSerGlyValSerSerSerThrSer......GlyGlyVal 55
                                                                                                                                                                                                                                                                                                                                                                              86 alAlaLysIleThrAlaGlnAlaThrGlyLysAspThrSerSerIleThr 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56 SerSerThrSer.....AsnMetHisGlySerLeuLeuGlnGluLy 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30 uAspSerSerCysLysGluSer.....SerValSerValT 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14 ThrCysSerSerAspAspArgGlyHisSerSerLeuThrAsnSerProLe
                                                                                                                                                       yAsnValValLysGlnGluGlnLeu............
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACAAGTACATCTGAATCTAACTCAATGCATCCGTCAGACTCAATGAGTAT 11809
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NAME: HOOVET, Kenley K.
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PB248P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171C
FILING DATE: 20-Oct-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                       TGACTCAATAAAACAAAATGGATTACTAGGTGGCGTTATGACATTATTAG
                                                                                                                                                                                                                AAACATAATGGCACACCAGCACAAAGTGAAAAAAGATTGCCAGATACAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sHisArgIleLeuHisLysLeuLeuGlnAsnGlyAsnSerProAlaGluV
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                                                .....SerProLysLysLysGluAsnAsnAlaLeu 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 13059 base pairs TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/009,861
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0.969
50.943
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Percent Identity: 25.157
                                                                                                                                                                                                                                                                 .....AspGl 107
                                                                                                                                                                115
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                                                                                                       11609
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; NAME/KEY: unsure ; LOCATION: (1)..(506113) ; OTHER INFORMATION: unsure at all n locations US-09-739-449-218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_block:
US-09-041-994-2_COPY_613_752 x US-09-739-449-218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: US-09-739-449-218 from: 1 to: 506113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NÜMBER: US/09/739,449
CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: US 09/514,000
PRIOR FILING DATE: 2000-02-23
NUMBER OF SEO ID NOS: 13351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Hinkle, Gregory J.

APPLICANT: Slater, Steven C.

TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15490)C
                                                                                                                                                                                                                                                                                                                                                 94962 TCCACCAATACCAGGCTGACACAGCTTCTAGCGCAATATGACCAGGCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                   94927 CCCTTCTCGGCTCC.....TATGGGCTCGACAGCTCTTCT
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                                                   95112 CTGAGCAAGGATCCGGACAAGGCATCGCAGGCCAACGCCATGCTGGAGGC
                                                                                                                                                   95062 ACATCACCAAGGCCGATTTCATGAAAGGGCTGAAGGGGATGCTGGAGGAG
                                                                                                                                                                                                                                                     95012
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
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     128 rLeu...
                                                                                                                                                                                                                                                                                                   94
                                                                                                                                                                                                                                                                                                                                                                                             81 AsnSerProAlaGluValAlaLysIleThrAla......GlnAlaTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64 erLeuLeuGlnGluLysHisArgIleLeuHisLysLeuLeuGlnAsnGly 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47 lSerSerSerThrSerGlyGlyValSerSerThrSerAsnMetHisGlyS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31 pSerSerCysLysGluSerSerVal.SerValThrSerProSerGly.Va 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15
                                                                                                                                                                                                                                                                                           rGlyLysAspThr...SerSerIleThrSerCys.....GlyAspGlyA 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CysSerSerAspAspArgGlyHisSerSerLeuThrAsnSerProLeuAs
                                                                                               LeuSer.....ProLysLysLysGluAsnAsnAlaLeuLeuArgTy
                                                                                                                                                                                                 snValValLysGln......GluGln 114
                                                                                                                                                                                                                                                     CGGCGACGACACACAGACCGAGGTCACGGATATGCAGCCTTCTTCCGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .TCGACCTTTCCACCCGCCTCACCGCCACCAGACTGGCCCTCAAGGCCAT
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0.857
60.667
.LeuAspArgAspAspProSerAspAlaLeu 139
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Percent Identity:
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10
27.333
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                                                      95161
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95162 CTTGAAGGCCGGCACGCTGACGGTCTCCGATCCCGACGGTTTA

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seq_documentation_block:
    Sequence 12219, Application US/09335032
    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_block:
US-09-041-994-2_COPY_613_752 x US-09-335-032-12216/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-335-032-12216
                                                                                                                                                                                                                                                                     seq_name: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to reverse of: US-09-335-032-12216 from: 1 to: 924430
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Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATIÓN:
APPLICANT: Velculescu, Victor
APPLICANT: Vogelstein, Bert
APPLICANT: Kinzler, Kenneth
                                                                                                                                                                                                                                                                                                                                                                                                                                                  879759 AGATTTAGAACAGTTGACTGGTTTTGACAACATCAGATTATATGGCGTTG 879710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               879814 CTTACAGTCCTTACAATGATGATGGGTCCTGT......879783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        879864 TTCATCCTCCGCTTCATCTAGTATCTCAGCCTCCGGTGCTAAGGGTATTA 879815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         879914 TCTTCGACCTCATCCTCATCCTCATCCTCAACTTCATCTTCAGC 879865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 12216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 12216, Application US/09335032
APPLICANT: Velculescu, Victor
APPLICANT: Vogelstein, Bert
APPLICANT: Kinzler, Kenneth
TITLE OF INVENTION: Characterization of the Yeast
TITLE OF INVENTION: Transcriptome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/035,917
PRIOR FILING DATE: 1997-01-23
PRIOR APPLICATION NUMBER: US 09/012,031
PRIOR FILING DATE: 1998-01-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Characterization of the Yeast TITLE OF INVENTION: Transcriptome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 12219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72 IleLeuHisLysLeuLeuGlnAsnGlyAsnSerProAlaGluValAlaLy 88
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                                                                                                                                                                                                                                                                                                                                                                     erCysGlyAspGlyAsnValValLysGlnGlnLeuSerProLysLys 119
                                                                                                                                                                                                                                                                                                                                ACTGTAGTCAGGTTGAGAATGTCTTGCAAGCTAAAACTTCAAGCCAGAAA 879660
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .....AAATCTACTGCTCAAGTCGCCTC 879760
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1.418
55.000
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12219
LENGTH: 948061
TYPE: DNA
ORGANISM: Saccharomyces cerevisiae
US-09-335-032-12219
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Ratio:
Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 295710 CCTGATGACATGATAAGCGAGGTTCCTTCTATTTCCGTG......
                                                                                              295431 ACCATTACGAAGCAAAGAGAAGAGGTGTCACCTCCAAATGTTGAAGCTGA 295382
                                                                                                                                                                                            295472 CGGATGCAGGCGGTAAGCTTACTGAA.....AAGTCATCAGAAGGC
                                                                                                                                                                                                                                                                                                295522 TTTTGCTGCTAATAGAATAGCCTTTGAAGTAGCCAATTTTAAGACTGCTT
                                                                                                                                                                                                                                                                                                                                                                                                   295572 AATCAAAAGTTGGCTTTAAGGGAGGCTGCTAAGCATCAGCAAGAAGCTCA 295523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  295622 AGGGACCGTTGTACACTAAGAAGTCTAAAGAATATATACTCGCCCTGGAA 295573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     295671 .GGTATTTCCAGTAGCAACCAATCGGCCAAGTCAACCAATTCCAACATTA 295623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/035,917
PRIOR FILING DATE: 1997-01-23
PRIOR APPLICATION NUMBER: US 09/012,031
PRIOR FILING DATE: 1998-01-22
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CURRENT APPLICATION NUMBER: US/09/335,032
CURRENT FILING DATE: 1999-06-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 isGlySerLeuLeuGlnGluLysHisArgIleLeuHisLysLeuLeuGln 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29 ProLeuAspSerSerCysLysGluSerSerValSerValThrSerProSe 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rGlyValSerSerSerThrSerGlyGlyValSerSerThrSerAsnMetH 62
TCGGGAGCTTGAGAATAATAAACTTGCAGAAAACCTC 295345
                                                                                                                                     AsnValValLysGln...GluGlnLeuSerPro......
                                                                                                                                                                                                                                                                                                                                       ......GlyAsnSerProAla...GluValAla.....LysIleThrA
                                                                                                                                                                                                                                                                                                                                                                                                                                                LysLysGluAsnAsnAlaLeuLeuArgTyrLeu 129
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1.187
51.938
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Gaps: 7
Percent Identity: 29.457
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